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Gerritsen,Mary E.
Goddard,Audrey
Godowski,Paul J.
Grimaldi,J.Christopher
Gurney,Austin L.
Kljavin,Ivar J.
Napier,Mary A.
Pan,James
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tgtatgtata agaatatttc tgacagtgag tgacccggag tctctggtgt 2700

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gacaaggcaa aacatgacag tggattctct ttacaaatgg aaaaaaaaaa 2950

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Leu Gly Leu Ile Ser Pro Ala Tyr Leu Phe Leu Trp Pro Glu Ala
             35                  40                  45

Phe Leu Tyr Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe
             50                  55                  60

Tyr Phe Pro Val Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn
             65                  70                  75

Leu Tyr Phe Leu Tyr Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala
             80                  85                  90

Phe Asp Gly Arg Pro Ala Asp Tyr Leu Phe Met Leu Leu Phe Asn
             95                 100                 105
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Trp Ile Cys Ile Val Ile Thr Gly Leu Ala Met Asp Met Gln Leu
110 115 120

Leu Met Ile Pro Leu Ile Met Ser Val Leu Tyr Val Trp Ala Gln
125 130 135

Leu Asn Arg Asp Met Ile Val Ser Phe Trp Phe Gly Thr Arg Phe
140 145 150

Lys Ala Cys Tyr Leu Pro Trp Val Ile Leu Gly Phe Asn Tyr Ile
155 160 165

Ile Gly Gly Ser Val Ile Asn Glu Leu Ile Gly Asn Leu Val Gly
170 175 180

His Leu Tyr Phe Phe Leu Met Phe Arg Tyr Pro Met Asp Leu Gly
185 190 195

Gly Arg Asn Phe Leu Ser Thr Pro Gln Phe Leu Tyr Arg Trp Leu
200 205 210

Pro Ser Arg Arg Gly Gly Val Ser Gly Phe Gly Val Pro Pro Ala
215 220 225

Ser Met Arg Arg Ala Ala Asp Gln Asn Gly Gly Gly Gly Arg His
230 235 240

Asn Trp Gly Gln Gly Phe Arg Leu Gly Asp Gln
245 250

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gtccggcggt ctggcctagg gatcttcccc gttgcccctt tggggcggga 200

tggctgcgga agaagaagac gaggtggagt gggtagtgga gagcatcgcg 250

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<213> Homo sapiens

<400> 8

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Asp Phe Val Glu Gln Lys Cys Glu Val Asn Cys Lys Gly Gly His
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Val Ile Thr Pro Gly Ser Pro Glu Pro Val Ile Leu Val Ala Cys
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Val Pro Leu Val Phe Asp Asp Glu Glu Glu Ser Lys Leu Thr Tyr
65 70 75

Thr Glu Ile His Gln Glu Tyr Lys Glu Leu Val Glu Lys Leu Leu
80 85 90

Glu Gly Tyr Leu Lys Glu Ile Gly Ile Asn Glu Asp Gln Phe Gln
95 100 105

Glu Ala Cys Thr Ser Pro Leu Ala Lys Thr His Thr Ser Gln Ala
110 115 120

Ile Leu Gln Pro Val Leu Ala Ala Glu Asp Phe Thr Ile Phe Lys
125 130 135

Ala Met Met Val Gln Lys Asn Ile Glu Met Gln Leu Gln Ala Ile
140 145 150

Arg Ile Ile Gln Glu Arg Asn Gly Val Leu Pro Asp Cys Leu Thr
155 160 165

Asp Gly Ser Asp Val Val Ser Asp Leu Glu His Glu Glu Met Lys
170 175 180

Ile Leu Arg Glu Val Leu Arg Lys Ser Lys Glu Glu Tyr Asp Gln
185 190 195

Glu Glu Glu Arg Lys Arg Lys Lys Gln Leu Ser Glu Ala Lys Thr
200 205 210

Glu Glu Pro Thr Val His Ser Ser Glu Ala Ala Ile Met Asn Asn
215 220 225

Ser Gln Gly Asp Gly Glu His Phe Ala His Pro Pro Ser Glu Val
230 235 240

Lys Met His Phe Ala Asn Gln Ser Ile Glu Pro Leu Gly Arg Lys
245 250 255

Val Glu Arg Ser Glu Thr Ser Ser Leu Pro Gln Lys Gly Leu Lys
260 265 270

Ile Pro Gly Leu Glu His Ala Ser Ile Glu Gly Pro Ile Ala Asn
275 280 285

Leu Ser Val Leu Gly Thr Glu Glu Leu Arg Gln Arg Glu His Tyr
290 295 300

Leu Lys Gln Lys Arg Asp Lys Leu Met Ser Met Arg Lys Asp Met
305 310 315

Arg Thr Lys Gln Ile Gln Asn Met Glu Gln Lys Gly Lys Pro Thr
320 325 330

Gly Glu Val Glu Glu Met Thr Glu Lys Pro Glu Met Thr Ala Glu
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Lys Glu Glu Val Ile Asn Lys
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tgcacttctc ctcttgcaaa gacccataca tcacaggcca tttttgcaac 200

ctgtgttggc agcagaagat tttactatct ttaaagcaat gatggtccag 250

aaaaacattg aaatgcagct gcaagccatt cgaataattc aagagagaaa 300

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<223> Synthetic oligonucleotide probe

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ctaagaactt ccctcaggat ttt 23

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<210> 13
<211> 2886
<212> DNA
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cactagaagc tcttctgagg gaggtaatta aaaaacagtg gaatggaaaa 200

acagtgctgt agtcatcctg taatatgctc cttgtcaaca atgtatacat 250

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<212> PRT
<213> Homo sapiens

<400> 14

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				20				25					30		
Ser	Ser	Arg	Ile	Leu	Leu	Val	Lys	Tyr	Ser	Ala	Asn	Glu	Glu	Asn	
				35				40					45		
Lys	Tyr	Asp	Tyr	Leu	Pro	Thr	Thr	Val	Asn	Val	Cys	Ser	Glu	Leu	
				50				55					60		
Val	Lys	Leu	Val	Phe	Cys	Val	Leu	Val	Ser	Phe	Cys	Val	Ile	Lys	
			.	65				70					75		
Lys	Asp	His	Gln	Ser	Arg	Asn	Leu	Lys	Tyr	Ala	Ser	Trp	Lys	Glu	
				80				85					90		
Phe	Ser	Asp	Phe	Met	Lys	Trp	Ser	Ile	Pro	Ala	Phe	Leu	Tyr	Phe	
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Leu	Asp	Asn	Leu	Ile	Val	Phe	Tyr	Val	Leu	Ser	Tyr	Leu	Gln	Pro	
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Ala Met Ala Val Ile Phe Ser Asn Phe Ser Ile Ile Thr Thr Ala
125 130 135

Leu Leu Phe Arg Ile Val Leu Lys Arg Arg Leu Asn Trp Ile Gln
140 145 150

Trp Ala Ser Leu Leu Thr Leu Phe Leu Ser Ile Val Ala Leu Thr
155 160 165

Ala Gly Thr Lys Thr Leu Gln His Asn Leu Ala Gly Arg Gly Phe
170 175 180

His His Asp Ala Phe Phe Ser Pro Ser Asn Ser Cys Leu Leu Phe
185 190 195

Arg Ser Glu Cys Pro Arg Lys Asp Asn Cys Thr Ala Lys Glu Trp
200 205 210

Thr Phe Pro Glu Ala Lys Trp Asn Thr Thr Ala Arg Val Phe Ser
215 220 225

His Ile Arg Leu Gly Met Gly His Val Leu Ile Ile Val Gln Cys
230 235 240

Phe Ile Ser Ser Met Ala Asn Ile Tyr Asn Glu Lys Ile Leu Lys
245 250 255

Glu Gly Asn Gln Leu Thr Glu Ser Ile Phe Ile Gln Asn Ser Lys
260 265 270

Leu Tyr Phe Phe Gly Ile Leu Phe Asn Gly Leu Thr Leu Gly Leu
275 280 285

Gln Arg Ser Asn Arg Asp Gln Ile Lys Asn Cys Gly Phe Phe Tyr
290 295 300

Gly His Ser Ala Phe Ser Val Ala Leu Ile Phe Val Thr Ala Phe
305 310 315

Gln Gly Leu Ser Val Ala Phe Ile Leu Lys Phe Leu Asp Asn Met
320 325 330

Phe His Val Leu Met Ala Gln Val Thr Thr Val Ile Ile Thr Thr
335 340 345

Val Ser Val Leu Val Phe Asp Phe Arg Pro Ser Leu Glu Phe Phe
350 355 360

Leu Glu Ala Pro Ser Val Leu Leu Ser Ile Phe Ile Tyr Asn Ala
365 370 375

Ser Lys Pro Gln Val Pro Glu Tyr Ala Pro Arg Gln Glu Arg Ile
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Arg Asp Leu Ser Gly Asn Leu Trp Glu Arg Ser Ser Gly Asp Gly
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<212> DNA
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<210> 19
<211> 2142
<212> DNA
<213> Homo sapiens

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<210> 20
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<212> PRT
<213> Homo sapiens

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Ala	Ser	Ala	Asn	Pro	Pro	Gly	Pro	Ala	Trp	Val	Ala	Leu	Cys	Pro	
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Gly	Ser	Ser	Ser	Pro	Arg	Pro	Trp	Pro	Ser	Leu	Pro	Thr	Ser	Ser	
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Ser	Gly	Ser	Cys	Pro	Thr	Ser	His	Thr	Ala	Arg	Pro	Ile	Gly	Thr	
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Cys	Phe	Ser	Ile	Ala	Ser	Leu	Lys	Gln	Trp	Ser	Arg	Val	Ser	Met	
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Phe	Pro	Thr	Arg	Leu	Ser	Pro	Cys	Ser	Ser	Ala	Thr	Glu	Gln	Thr	
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Gly Thr Val Leu Gly Thr Ala Ile Gln Gly Gln Ile Val Gly Gln
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140 145 150

Ser Gln Ser Ala Asn His Thr His Gly Thr Thr Ser His Arg Glu
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Thr Gln Lys Ala Tyr Leu Leu Ala Ala Gly Val Ile Val Cys Ile
170 175 180

Tyr Ile Ile Cys Ala Val Ile Leu Ile Leu Gly Val Arg Glu Gln
185 190 195

Arg Glu Pro Tyr Glu Ala Gln Gln Ser Glu Pro Ile Ala Tyr Phe
200 205 210

Arg Gly Leu Arg Leu Val Met Ser His Gly Pro Tyr Ile Lys Leu
215 220 225

Ile Thr Gly Phe Leu Phe Thr Ser Leu Ala Phe Met Leu Val Glu
230 235 240

Gly Asn Phe Val Leu Phe Cys Thr Tyr Thr Leu Gly Phe Arg Asn
245 250 255

Glu Phe Gln Asn Leu Leu Leu Ala Ile Met Leu Ser Ala Thr Leu
260 265 270

Thr Ile Pro Ile Trp Gln Trp Phe Leu Thr Arg Phe Gly Lys Lys
275 280 285

Thr Ala Val Tyr Val Gly Ile Ser Ser Ala Val Pro Phe Leu Ile
290 295 300

Leu Val Ala Leu Met Glu Ser Asn Leu Ile Ile Thr Tyr Ala Val
305 310 315

Ala Val Ala Ala Gly Ile Ser Val Ala Ala Ala Phe Leu Leu Pro
320 325 330

Trp Ser Met Leu Pro Asp Val Ile Asp Asp Phe His Leu Lys Gln
335 340 345

Pro His Phe His Gly Thr Glu Pro Ile Phe Phe Ser Phe Tyr Val
350 355 360

Phe Phe Thr Lys Phe Ala Ser Gly Val Ser Leu Gly Ile Ser Thr
365 370 375

Leu Ser Leu Asp Phe Ala Gly Tyr Gln Thr Arg Gly Cys Ser Gln
380 385 390

Pro Glu Arg Val Lys Phe Thr Leu Asn Met Leu Val Thr Met Ala
395 400 405

Pro Ile Val Leu Ile Leu Leu Gly Leu Leu Leu Phe Lys Met Tyr
410 415 420

Pro Ile Asp Glu Glu Arg Arg Arg Gln Asn Lys Lys Ala Leu Gln
425 430 435

Ala Leu Arg Asp Glu Ala Ser Ser Ser Gly Cys Ser Glu Thr Asp
440 445 450

Ser Thr Glu Leu Ala Ser Ile Leu
455

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<211> 571
<212> DNA
<213> Homo sapiens

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accctatgaa gcccagcagt ctgagccaat cgcctacttc cggggcctac 150

ggctggtcat gagccacggc ccatacatca aacttattac tggcttcctc 200

ttcacctcct tggctttcat gctggtggag gggaactttg tcttgttttg 250

cacctacacc ttgggcttcc gcaatgaatt ccagaatcta ctcctggcca 300

tcatgctctc ggccacttta accattccca tctggcagtg gttcttgacc 350

cggtttggca agaagacagc tgtatatgtt gggatctcat cagcagtgcc 400

atttctcatc ttggtggccc tcatggagag taacctcatc attacatatg 450

cggtagctgt ggcagctggc atcagtgtgg cagctgcctt cttactaccc 500

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cttccatgga accgagccca t 571

<210> 22
<211> 1173
<212> DNA
<213> Homo sapiens

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aaacagaaaa cctgttagaa atgtggtggt ttcagcaagg cctcagtttc 150

cttccttcag cccttgtaat ttggacatct gctgctttca tattttcata 200

cattactgca gtaacactcc accatataga cccggcttta ccttatatca 250

gtgacactgg tacagtagct ccagaaaaat gcttatttgg ggcaatgcta 300

aatattgcgg cagttttatg cattgctacc atttatgttc gttataagca 350

agttcatgct ctgagtcctg aagagaacgt tatcatcaaa ttaaacaagg 400

ctggccttgt acttggaata ctgagttgtt taggactttc tattgtggca 450

aacttccaga aaacaaccct ttttgctgca catgtaagtg gagctgtgct 500

tacctttggt atgggctcat tatatatgtt tgttcagacc atcctttcct 550

accaaatgca gcccaaaatc catggcaaac aagtcttctg gatcagactg 600

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atcagttttg cacagtggca attttgggac tgatttagaa cagaaactcc 700

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taaccctcta tgacactgca ccttgcccta ttaacaatga acgaacacgg 900

ctactttcca gagatatttg atgaaaggat aaaatatttc tgtaatgatt 950

atgattctca gggattgggg aaaggttcac agaagttgct tattcttctc 1000

tgaaattttc aaccacttaa tcaaggctga cagtaacact gatgaatgct 1050

gataatcagg aaacatgaaa gaagccattt gatagattat tctaaaggat 1100

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gaaaataaag tcaaaagact atg 1173

<210> 23
<211> 266
<212> PRT
<213> Homo sapiens

<400> 23

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Val Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala
             20                  25                  30

Val Thr Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp
             35                  40                  45

Thr Gly Thr Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu
             50                  55                  60

Asn Ile Ala Ala Val Leu Cys Ile Ala Thr Ile Tyr Val Arg Tyr
             65                  70                  75

Lys Gln Val His Ala Leu Ser Pro Glu Glu Asn Val Ile Ile Lys
             80                  85                  90

Leu Asn Lys Ala Gly Leu Val Leu Gly Ile Leu Ser Cys Leu Gly
             95                 100                 105

Leu Ser Ile Val Ala Asn Phe Gln Lys Thr Thr Leu Phe Ala Ala
            110                 115                 120

His Val Ser Gly Ala Val Leu Thr Phe Gly Met Gly Ser Leu Tyr
            125                 130                 135
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Met Phe Val Gln Thr Ile Leu Ser Tyr Gln Met Gln Pro Lys Ile
140 145 150

His Gly Lys Gln Val Phe Trp Ile Arg Leu Leu Leu Val Ile Trp
155 160 165

Cys Gly Val Ser Ala Leu Ser Met Leu Thr Cys Ser Ser Val Leu
170 175 180

His Ser Gly Asn Phe Gly Thr Asp Leu Glu Gln Lys Leu His Trp
185 190 195

Asn Pro Glu Asp Lys Gly Tyr Val Leu His Met Ile Thr Thr Ala
200 205 210

Ala Glu Trp Ser Met Ser Phe Ser Phe Phe Gly Phe Phe Leu Thr
215 220 225

Tyr Ile Arg Asp Phe Gln Lys Ile Ser Leu Arg Val Glu Ala Asn
230 235 240

Leu His Gly Leu Thr Leu Tyr Asp Thr Ala Pro Cys Pro Ile Asn
245 250 255

Asn Glu Arg Thr Arg Leu Leu Ser Arg Asp Ile
260 265

<210> 24
<211> 485
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 14, 484
<223> unknown base

<400> 24
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gagcggagat cctcaaacgg cctagtgctt cgcgcttccg gagaaaatca 150

gcggtctaat taattcctct ggtttgttga agcagttacc aagaatcttc 200

aacccttttcc cacaaaagct aattgagtac acgttcctgt tgagtacacg 250

ttcctgttga tttacaaaag gtgcaggtat gagcaggtct gaagactaac 300

attttgtgaa gttgtaaaac agaaaacctg ttagaaatgt ggtggtttca 350

gcaaggcctc agtttccttc cttcagccct tgtaatttgg acatctgctg 400

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<210> 25
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
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<210> 26
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
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<210> 27
<211> 1399
<212> DNA
<213> Homo sapiens

<400> 27
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ctgccccgcg ggccggggtg cggagccgac atgcgcccgc ttctcggcct 100

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gactgccccg cgggcggaga ctgggctcca ccgaggaggc tggaggcagg 200

tcgctgtggt tcccctccga cctggcagag ctgcgggagc tctctgaggt 250

ccttcgagag taccggaagg agcaccaggc ctacgtgttc ctgctcttct 300

gcggcgccta cctctacaaa cagggctttg ccatccccgg ctccagcttc 350

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gtgctgtgtg ttgacctcgg tgggtgccac atgctgctac ctgctctcca 450

gtatttttgg caaacagttg gtggtgtcct actttcctga taaagtggcc 500

ctgctgcaga gaaaggtgga ggagaacaga aacagcttgt ttttttcctt 550

attgtttttg agacttttcc ccatgacacc aaactggttc ttgaacctct 600

cggccccaat tctgaacatt cccatcgtgc agttcttctt ctcagttctt 650

atcggtttga tcccatataa tttcatctgt gtgcagacag ggtccatcct 700

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gccaggcgtg gtggcaggca cctgtaatcc cagctactcg ggaggctgag 1300

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cacaccactg cactccagcc tgggtgatag agtgagacac tgtcttgac 1399

<210> 28
<211> 264
<212> PRT
<213> Homo sapiens

<400> 28

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Phe	Ala	Leu	Tyr	Leu	Leu	Ser	Thr	Arg	Leu	Pro	Arg	Gly	Arg	Arg	
			20					25						30	
Leu	Gly	Ser	Thr	Glu	Glu	Ala	Gly	Gly	Arg	Ser	Leu	Trp	Phe	Pro	
			35					40						45	
Ser	Asp	Leu	Ala	Glu	Leu	Arg	Glu	Leu	Ser	Glu	Val	Leu	Arg	Glu	
			50					55						60	
Tyr	Arg	Lys	Glu	His	Gln	Ala	Tyr	Val	Phe	Leu	Leu	Phe	Cys	Gly	
			65					70						75	
Ala	Tyr	Leu	Tyr	Lys	Gln	Gly	Phe	Ala	Ile	Pro	Gly	Ser	Ser	Phe	
			80					85						90	
Leu	Asn	Val	Leu	Ala	Gly	Ala	Leu	Phe	Gly	Pro	Trp	Leu	Gly	Leu	
			95					100						105	
Leu	Leu	Cys	Cys	Val	Leu	Thr	Ser	Val	Gly	Ala	Thr	Cys	Cys	Tyr	
			110					115						120	
Leu	Leu	Ser	Ser	Ile	Phe	Gly	Lys	Gln	Leu	Val	Val	Ser	Tyr	Phe	
			125					130						135	
Pro	Asp	Lys	Val	Ala	Leu	Leu	Gln	Arg	Lys	Val	Glu	Glu	Asn	Arg	
			140					145						150	
Asn	Ser	Leu	Phe	Phe	Phe	Leu	Leu	Phe	Leu	Arg	Leu	Phe	Pro	Met	
			155					160						165	
Thr	Pro	Asn	Trp	Phe	Leu	Asn	Leu	Ser	Ala	Pro	Ile	Leu	Asn	Ile	
			170					175						180	
Pro	Ile	Val	Gln	Phe	Phe	Phe	Ser	Val	Leu	Ile	Gly	Leu	Ile	Pro	
			185					190						195	
Tyr	Asn	Phe	Ile	Cys	Val	Gln	Thr	Gly	Ser	Ile	Leu	Ser	Thr	Leu	
			200					205						210	

Thr Ser Leu Asp Ala Leu Phe Ser Trp Asp Thr Val Phe Lys Leu
215 220 225

Leu Ala Ile Ala Met Val Ala Leu Ile Pro Gly Thr Leu Ile Lys
230 235 240

Lys Phe Ser Gln Lys His Leu Gln Leu Asn Glu Thr Ser Thr Ala
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Asn His Ile His Ser Arg Lys Asp Thr
260

<210> 29
<211> 1292
<212> DNA
<213> Homo sapiens

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ggtttccgaa ctgccagctc agaataggaa aataacttgg gattttatat 150

tggaagacat ggatcttgct gccaacgaga tcagcattta tgacaaactt 200

tcagagactg ttgatttggt gagacagacc ggccatcagt gtggcatgtc 250

agagaaggca attgaaaaat ttatcagaca gctgctggaa aagaatgaac 300

ctcagagacc ccccccgcag tatcctctcc ttatagttgt gtataaggtt 350

ctcgcaacct tgggattaat cttgctcact gcctactttg tgattcaacc 400

tttcagccca ttagcacctg agccagtgct ttctggagct cacacctggc 450

gctcactcat ccatcacatt aggctgatgt ccttgcccat tgccaagaag 500

tacatgtcag aaaataaggg agttcctctg catgggggtg atgaagacag 550

acccctttcca gactttgacc cctggtggac aaacgactgt gagcagaatg 600

agtcagagcc cattcctgcc aactgcactg gctgtgccca gaaacacctg 650

aaggtgatgc tcctggaaga cgccccaagg aaatttgaga ggctccatcc 700

actggtgatc aagacgggaa agcccctgtt ggaggaagag attcagcatt 750

ttttgtgcca gtaccctgag gcgacagaag gcttctctga agggtttttc 800

gccaagtggt ggcgctgctt tcctgagcgg tggttcccat ttccttatcc 850

atggaggaga cctctgaaca gatcacaaat gttacgtgag ctttttcctg 900

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cctatttatc attggcagcg gtgaggccat gttgcagctc atccctccct 1050

tccagtgccg aagacattgt cagtctgtgg ccatgccaat agagccaggg 1100

gatatcggct atgtcgacac cacccactgg aaggtctacg ttatagccag 1150

aggggtccag cctttggtca tctgcgatgg aaccgctttc tcagaactgt 1200

aggaaataga actgtgcaca ggaacagctt ccagagccga aaaccaggtt 1250

gaaaggggaa aaataaaaac aaaaacgatg aaactgcaaa aa 1292

<210> 30
<211> 347
<212> PRT
<213> Homo sapiens

<400> 30

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Glu	Thr	Val	Asp	Leu	Val	Arg	Gln	Thr	Gly	His	Gln	Cys	Gly	Met	
			20					25						30	
Ser	Glu	Lys	Ala	Ile	Glu	Lys	Phe	Ile	Arg	Gln	Leu	Leu	Glu	Lys	
			35					40						45	
Asn	Glu	Pro	Gln	Arg	Pro	Pro	Pro	Gln	Tyr	Pro	Leu	Leu	Ile	Val	
			50					55						60	
Val	Tyr	Lys	Val	Leu	Ala	Thr	Leu	Gly	Leu	Ile	Leu	Leu	Thr	Ala	
			65					70						75	
Tyr	Phe	Val	Ile	Gln	Pro	Phe	Ser	Pro	Leu	Ala	Pro	Glu	Pro	Val	
			80					85						90	
Leu	Ser	Gly	Ala	His	Thr	Trp	Arg	Ser	Leu	Ile	His	His	Ile	Arg	
			95					100						105	
Leu	Met	Ser	Leu	Pro	Ile	Ala	Lys	Lys	Tyr	Met	Ser	Glu	Asn	Lys	
			110					115						120	
Gly	Val	Pro	Leu	His	Gly	Gly	Asp	Glu	Asp	Arg	Pro	Phe	Pro	Asp	
			125					130						135	
Phe	Asp	Pro	Trp	Trp	Thr	Asn	Asp	Cys	Glu	Gln	Asn	Glu	Ser	Glu	
			140					145						150	
Pro	Ile	Pro	Ala	Asn	Cys	Thr	Gly	Cys	Ala	Gln	Lys	His	Leu	Lys	
			155					160						165	
Val	Met	Leu	Leu	Glu	Asp	Ala	Pro	Arg	Lys	Phe	Glu	Arg	Leu	His	
			170					175						180	
Pro	Leu	Val	Ile	Lys	Thr	Gly	Lys	Pro	Leu	Leu	Glu	Glu	Glu	Ile	
			185					190						195	
Gln	His	Phe	Leu	Cys	Gln	Tyr	Pro	Glu	Ala	Thr	Glu	Gly	Phe	Ser	
			200					205						210	
Glu	Gly	Phe	Phe	Ala	Lys	Trp	Trp	Arg	Cys	Phe	Pro	Glu	Arg	Trp	
			215					220						225	
Phe	Pro	Phe	Pro	Tyr	Pro	Trp	Arg	Arg	Pro	Leu	Asn	Arg	Ser	Gln	
			230					235						240	
Met	Leu	Arg	Glu	Leu	Phe	Pro	Val	Phe	Thr	His	Leu	Pro	Phe	Pro	
			245					250						255	

Lys Asp Ala Ser Leu Asn Lys Cys Ser Phe Leu His Pro Glu Pro
260 265 270

Val Val Gly Ser Lys Met His Lys Met Pro Asp Leu Phe Ile Ile
275 280 285

Gly Ser Gly Glu Ala Met Leu Gln Leu Ile Pro Pro Phe Gln Cys
290 295 300

Arg Arg His Cys Gln Ser Val Ala Met Pro Ile Glu Pro Gly Asp
305 310 315

Ile Gly Tyr Val Asp Thr Thr His Trp Lys Val Tyr Val Ile Ala
320 325 330

Arg Gly Val Gln Pro Leu Val Ile Cys Asp Gly Thr Ala Phe Ser
335 340 345

Glu Leu

<210> 31
<211> 478
<212> DNA
<213> Homo sapiens

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cgcagtatcc tctccttata gttgtgtata aggttctcgc aaccttggga 400

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acctgagcca gtgctttgtg gagctcac 478

<210> 32
<211> 3531
<212> DNA
<213> Homo sapiens

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cttcctggag aaccagaacg gttttgacct gggctgtctc cagctgacca 1850

acgagaaggt aggcgatgtg gtgctacccc cgtgggccag ctctcctgag 1900

gacttcatcc agcagcaccg ccaggctctg gagtcggagt atgtgtctgc 1950

acacctacac gagtggatcg acctcatctt tggctacaag cagcgggggc 2000

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gaaagctgct attcagcggt ggccactggg atggcagcct gcgggtgact 2500

gcactacccc gtggcaagct gttgagccag ctcagctgcc accttgatgt 2550

agtaacctgc cttgcactgg acacctgtgg catctacctc atctcaggct 2600

cccgggacac cacgtgcatg gtgtggcggc tcctgcatca gggtggtctg 2650

tcagtaggcc tggcaccaaa gcctgtgcag gtcctgtatg ggcatggggc 2700

tgcagtgagc tgtgtggcca tcagcactga acttgacatg gctgtgtctg 2750

gatctgagga tggaactgtg atcatacaca ctgtacgccg cggacagttt 2800

gtagcggcac tacggcctct gggtgccaca ttccctggac ctattttcca 2850

cctggcattg gggtccgaag gccagattgt ggtacagagc tcagcgtggg 2900

aacgtcctgg ggcccaggtc acctactcct tgcacctgta ttcagtcaat 2950

gggaagttgc gggcttcact gcccctggca gagcagccta cagccctgac 3000

ggtgacagag gactttgtgt tgctgggcac cgcccagtgc gccctgcaca 3050

tcctccaact aaacacactg ctcccggccg cgcctccctt gcccatgaag 3100

gtggccatcc gcagcgtggc cgtgaccaag gagcgcagcc acgtgctggt 3150

gggcctggag gatggcaagc tcatcgtggt ggtcgcgggg cagccctctg 3200

aggtgcgcag cagccagttc gcgcggaagc tgtggcggtc ctcgcggcgc 3250

atctcccagg tgtcctcggg agagacggaa tacaacccta ctgaggcgcg 3300

ctgaacctgg ccagtccggc tgctcgggcc ccgcccccgg caggcctggc 3350

ccgggaggcc ccgcccagaa gtcggcggga acaccccggg gtgggcagcc 3400

caggggggtga gcggggccca ccctgcccag ctcagggatt ggcgggcgat 3450

gttacccccc cagggattgg cgggcggaag tcccgccccc cgccggctga 3500

ggggccgccc tgagggccag cactggcgtc t 3531

<210> 33
<211> 1003
<212> PRT
<213> Homo sapiens

<400> 33

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Met Ser Gln Phe Glu Met Asp Thr Tyr Ala Lys Ser His Asp Leu
  1               5                  10                  15

Met Ser Gly Phe Trp Asn Ala Cys Tyr Asp Met Leu Met Ser Ser
             20                  25                  30

Gly Gln Arg Arg Gln Trp Glu Arg Ala Gln Ser Arg Arg Ala Phe
             35                  40                  45

Gln Glu Leu Val Leu Glu Pro Ala Gln Arg Arg Ala Arg Leu Glu
             50                  55                  60

Gly Leu Arg Tyr Thr Ala Val Leu Lys Gln Gln Ala Thr Gln His
             65                  70                  75

Ser Met Ala Leu Leu His Trp Gly Ala Leu Trp Arg Gln Leu Ala
             80                  85                  90

Ser Pro Cys Gly Ala Trp Ala Leu Arg Asp Thr Pro Ile Pro Arg
             95                 100                 105

Trp Lys Leu Ser Ser Ala Glu Thr Tyr Ser Arg Met Arg Leu Lys
            110                 115                 120

Leu Val Pro Asn His His Phe Asp Pro His Leu Glu Ala Ser Ala
            125                 130                 135

Leu Arg Asp Asn Leu Gly Glu Val Pro Leu Thr Pro Thr Glu Glu
            140                 145                 150

Ala Ser Leu Pro Leu Ala Val Thr Lys Glu Ala Lys Val Ser Thr
            155                 160                 165

Pro Pro Glu Leu Leu Gln Glu Asp Gln Leu Gly Glu Asp Glu Leu
            170                 175                 180

Ala Glu Leu Glu Thr Pro Met Glu Ala Ala Glu Leu Asp Glu Gln
            185                 190                 195

Arg Glu Lys Leu Val Leu Ser Ala Glu Cys Gln Leu Val Thr Val
            200                 205                 210

Val Ala Val Val Pro Gly Leu Leu Glu Val Thr Thr Gln Asn Val
            215                 220                 225

Tyr Phe Tyr Asp Gly Ser Thr Glu Arg Val Glu Thr Glu Glu Gly
            230                 235                 240

Ile Gly Tyr Asp Phe Arg Arg Pro Leu Ala Gln Leu Arg Glu Val
            245                 250                 255

His Leu Arg Arg Phe Asn Leu Arg Arg Ser Ala Leu Glu Leu Phe
            260                 265                 270
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Phe Ile Asp Gln Ala Asn Tyr Phe Leu Asn Phe Pro Cys Lys Val
275 280 285

Gly Thr Thr Pro Val Ser Ser Pro Ser Gln Thr Pro Arg Pro Gln
290 295 300

Pro Gly Pro Ile Pro Pro His Thr Gln Val Arg Asn Gln Val Tyr
305 310 315

Ser Trp Leu Leu Arg Leu Arg Pro Pro Ser Gln Gly Tyr Leu Ser
320 325 330

Ser Arg Ser Pro Gln Glu Met Leu Arg Ala Ser Gly Leu Thr Gln
335 340 345

Lys Trp Val Gln Arg Glu Ile Ser Asn Phe Glu Tyr Leu Met Gln
350 355 360

Leu Asn Thr Ile Ala Gly Arg Thr Tyr Asn Asp Leu Ser Gln Tyr
365 370 375

Pro Val Phe Pro Trp Val Leu Gln Asp Tyr Val Ser Pro Thr Leu
380 385 390

Asp Leu Ser Asn Pro Ala Val Phe Arg Asp Leu Ser Lys Pro Ile
395 400 405

Gly Val Val Asn Pro Lys His Ala Gln Leu Val Arg Glu Lys Tyr
410 415 420

Glu Ser Phe Glu Asp Pro Ala Gly Thr Ile Asp Lys Phe His Tyr
425 430 435

Gly Thr His Tyr Ser Asn Ala Ala Gly Val Met His Tyr Leu Ile
440 445 450

Arg Val Glu Pro Phe Thr Ser Leu His Val Gln Leu Gln Ser Gly
455 460 465

Arg Phe Asp Cys Ser Asp Arg Gln Phe His Ser Val Ala Ala Ala
470 475 480

Trp Gln Ala Arg Leu Glu Ser Pro Ala Asp Val Lys Glu Leu Ile
485 490 495

Pro Glu Phe Phe Tyr Phe Pro Asp Phe Leu Glu Asn Gln Asn Gly
500 505 510

Phe Asp Leu Gly Cys Leu Gln Leu Thr Asn Glu Lys Val Gly Asp
515 520 525

Val Val Leu Pro Pro Trp Ala Ser Ser Pro Glu Asp Phe Ile Gln
530 535 540

Gln His Arg Gln Ala Leu Glu Ser Glu Tyr Val Ser Ala His Leu
545 550 555

His Glu Trp Ile Asp Leu Ile Phe Gly Tyr Lys Gln Arg Gly Pro
560 565 570

Ala Ala Glu Glu Ala Leu Asn Val Phe Tyr Tyr Cys Thr Tyr Glu
575 580 585

Gly Ala Val Asp Leu Asp His Val Thr Asp Glu Arg Glu Arg Lys
590 595 600

Ala Leu Glu Gly Ile Ile Ser Asn Phe Gly Gln Thr Pro Cys Gln
605 610 615

Leu Leu Lys Glu Pro His Pro Thr Arg Leu Ser Ala Glu Glu Ala
620 625 630

Ala His Arg Leu Ala Arg Leu Asp Thr Asn Ser Pro Ser Ile Phe
635 640 645

Gln His Leu Asp Glu Leu Lys Ala Phe Phe Ala Glu Val Thr Val
650 655 660

Ser Ala Ser Gly Leu Leu Gly Thr His Ser Trp Leu Pro Tyr Asp
665 670 675

Arg Asn Ile Ser Asn Tyr Phe Ser Phe Ser Lys Asp Pro Thr Met
680 685 690

Gly Ser His Lys Thr Gln Arg Leu Leu Ser Gly Pro Trp Val Pro
695 700 705

Gly Ser Gly Val Ser Gly Gln Ala Leu Ala Val Ala Pro Asp Gly
710 715 720

Lys Leu Leu Phe Ser Gly Gly His Trp Asp Gly Ser Leu Arg Val
725 730 735

Thr Ala Leu Pro Arg Gly Lys Leu Leu Ser Gln Leu Ser Cys His
740 745 750

Leu Asp Val Val Thr Cys Leu Ala Leu Asp Thr Cys Gly Ile Tyr
755 760 765

Leu Ile Ser Gly Ser Arg Asp Thr Thr Cys Met Val Trp Arg Leu
770 775 780

Leu His Gln Gly Gly Leu Ser Val Gly Leu Ala Pro Lys Pro Val
785 790 795

Gln Val Leu Tyr Gly His Gly Ala Ala Val Ser Cys Val Ala Ile
800 805 810

Ser Thr Glu Leu Asp Met Ala Val Ser Gly Ser Glu Asp Gly Thr
815 820 825

Val Ile Ile His Thr Val Arg Arg Gly Gln Phe Val Ala Ala Leu
830 835 840

Arg Pro Leu Gly Ala Thr Phe Pro Gly Pro Ile Phe His Leu Ala
845 850 855

Leu Gly Ser Glu Gly Gln Ile Val Val Gln Ser Ser Ala Trp Glu
860 865 870

Arg Pro Gly Ala Gln Val Thr Tyr Ser Leu His Leu Tyr Ser Val
875 880 885

Asn Gly Lys Leu Arg Ala Ser Leu Pro Leu Ala Glu Gln Pro Thr
890 895 900

Ala Leu Thr Val Thr Glu Asp Phe Val Leu Leu Gly Thr Ala Gln
905 910 915

Cys Ala Leu His Ile Leu Gln Leu Asn Thr Leu Leu Pro Ala Ala
920 925 930

Pro Pro Leu Pro Met Lys Val Ala Ile Arg Ser Val Ala Val Thr
935 940 945

Lys Glu Arg Ser His Val Leu Val Gly Leu Glu Asp Gly Lys Leu
950 955 960

Ile Val Val Val Ala Gly Gln Pro Ser Glu Val Arg Ser Ser Gln
965 970 975

Phe Ala Arg Lys Leu Trp Arg Ser Ser Arg Arg Ile Ser Gln Val
980 985 990

Ser Ser Gly Glu Thr Glu Tyr Asn Pro Thr Glu Ala Arg
995 1000

<210> 34
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 34
tgactgcact accccgtggc aagctgttga gccagctcag ctg 43

<210> 35
<211> 1395
<212> DNA
<213> Homo sapiens

<400> 35
cggacgcgtg ggcggacgcg tgggggctgt gagaaagtgc caataaatac 50

atcatgcaac cccacggccc accttgtgaa ctcctcgtgc ccagggctga 100

tgtgcgtctt ccagggctac tcatccaaag gcctaatcca acgttctgtc 150

ttcaatctgc aaatctatgg ggtcctgggg ctcttctgga cccttaactg 200

ggtactggcc ctgggccaat gcgtcctcgc tggagccttt gcctccttct 250

actgggcctt ccacaagccc caggacatcc ctaccttccc cttaatctct 300

gccttcatcc gcacactccg ttaccacact gggtcattgg catttggagc 350

cctcatcctg acccttgtgc agatagcccg ggtcatcttg gagtatattg 400

accacaagct cagaggagtg cagaaccctg tagcccgctg catcatgtgc 450

tgtttcaagt gctgcctctg gtgtctggaa aaatttatca agttcctaaa 500

ccgcaatgca tacatcatga tcgccatcta cgggaagaat ttctgtgtct 550

cagccaaaaa tgcgttcatg ctactcatgc gaaacattgt cagggtggtc 600

gtcctggaca aagtcacaga cctgctgctg ttctttggga agctgctggt 650

ggtcggaggc gtgggggtcc tgtccttctt ttttttctcc ggtcgcatcc 700

cggggctggg taaagacttt aagagccccc acctcaacta ttactggctg 750

cccatcatga cctccatcct gggggcctat gtcatcgcca gcggcttctt 800

cagcgttttc ggcatgtgtg tggacacgct cttcctctgc ttcctggaag 850

acctggagcg gaacaacggc tccctggacc ggccctacta catgtccaag 900

agccttctaa agattctggg caagaagaac gaggcgcccc cggacaacaa 950

gaagaggaag aagtgacagc tccggccctg atccaggact gcaccccacc 1000

cccaccgtcc agccatccaa cctcacttcg ccttacaggt ctccattttg 1050

tggtaaaaaa aggttttagg ccaggcgccg tggctcacgc ctgtaatcca 1100

acactttgag aggctgaggc gggcggatca cctgagtcag gagttcgaga 1150

ccagcctggc caacatggtg aaacctccgt ctctattaaa aatacaaaaa 1200

ttagccgaga gtggtggcat gcacctgtca tcccagctac tcgggaggct 1250

gaggcaggag aatcgcttga acccgggagg cagaggttgc agtgagccga 1300

gatcgcgcca ctgcactcca acctgggtga cagactctgt ctccaaaaca 1350

aaacaaacaa acaaaaagat tttattaaag atattttgtt aactc 1395

<210> 36
<211> 321
<212> PRT
<213> Homo sapiens

<400> 36

Arg	Thr	Arg	Gly	Arg	Thr	Arg	Gly	Gly	Cys	Glu	Lys	Val	Pro	Ile	
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Asn	Thr	Ser	Cys	Asn	Pro	Thr	Ala	His	Leu	Val	Asn	Ser	Ser	Cys	
				20					25					30	
Pro	Gly	Leu	Met	Cys	Val	Phe	Gln	Gly	Tyr	Ser	Ser	Lys	Gly	Leu	
				35					40					45	
Ile	Gln	Arg	Ser	Val	Phe	Asn	Leu	Gln	Ile	Tyr	Gly	Val	Leu	Gly	
				50					55					60	
Leu	Phe	Trp	Thr	Leu	Asn	Trp	Val	Leu	Ala	Leu	Gly	Gln	Cys	Val	
				65					70					75	
Leu	Ala	Gly	Ala	Phe	Ala	Ser	Phe	Tyr	Trp	Ala	Phe	His	Lys	Pro	
				80					85					90	
Gln	Asp	Ile	Pro	Thr	Phe	Pro	Leu	Ile	Ser	Ala	Phe	Ile	Arg	Thr	
				95					100					105	
Leu	Arg	Tyr	His	Thr	Gly	Ser	Leu	Ala	Phe	Gly	Ala	Leu	Ile	Leu	
				110					115					120	
Thr	Leu	Val	Gln	Ile	Ala	Arg	Val	Ile	Leu	Glu	Tyr	Ile	Asp	His	
				125					130					135	

Lys Leu Arg Gly Val Gln Asn Pro Val Ala Arg Cys Ile Met Cys
140 145 150

Cys Phe Lys Cys Cys Leu Trp Cys Leu Glu Lys Phe Ile Lys Phe
155 160 165

Leu Asn Arg Asn Ala Tyr Ile Met Ile Ala Ile Tyr Gly Lys Asn
170 175 180

Phe Cys Val Ser Ala Lys Asn Ala Phe Met Leu Leu Met Arg Asn
185 190 195

Ile Val Arg Val Val Val Leu Asp Lys Val Thr Asp Leu Leu Leu
200 205 210

Phe Phe Gly Lys Leu Leu Val Val Gly Gly Val Gly Val Leu Ser
215 220 225

Phe Phe Phe Phe Ser Gly Arg Ile Pro Gly Leu Gly Lys Asp Phe
230 235 240

Lys Ser Pro His Leu Asn Tyr Tyr Trp Leu Pro Ile Met Thr Ser
245 250 255

Ile Leu Gly Ala Tyr Val Ile Ala Ser Gly Phe Phe Ser Val Phe
260 265 270

Gly Met Cys Val Asp Thr Leu Phe Leu Cys Phe Leu Glu Asp Leu
275 280 285

Glu Arg Asn Asn Gly Ser Leu Asp Arg Pro Tyr Tyr Met Ser Lys
290 295 300

Ser Leu Leu Lys Ile Leu Gly Lys Lys Asn Glu Ala Pro Pro Asp
305 310 315

Asn Lys Lys Arg Lys Lys
320

<210> 37
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 37
tcgtgcccag gggctgatgt gc 22

<210> 38
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 38
gtctttaccc agccccggga tgcg 24

<210> 39
<211> 50

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 39
ggcctaatcc aacgttctgt cttcaatctg caaatctatg gggtcctggg 50

<210> 40
<211> 1365
<212> DNA
<213> Homo sapiens

<400> 40
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tccggccgcc gtggctatgt tcgtgtccga tttccgcaaa gagttctacg 100

aggtggtcca gagccagagg gtccttctct tcgtggcctc ggacgtggat 150

gctctgtgtg cgtgcaagat ccttcaggcc ttgttccagt gtgaccacgt 200

gcaatatacg ctggttccag tttctgggtg gcaagaactt gaaactgcat 250

ttcttgagca taaagaacag tttcattatt ttattctcat aaactgtgga 300

gctaatgtag acctattgga tattcttcaa cctgatgaag acactatatt 350

ctttgtgtgt gactcccata ggccagtcaa tgtcgtcaat gtatacaacg 400

atacccagat caaattactc attaaacaag atgatgacct tgaagttccc 450

gcctatgaag acatcttcag ggatgaagag gaggatgaag agcattcagg 500

aaatgacagt gatgggtcag agccttctga gaagcgcaca cggttagaag 550

aggagatagt ggagcaaacc atgcggagga ggcagcggcg agagtgggag 600

gcccggagaa gagacatcct ctttgactac gagcagtatg aatatcatgg 650

gacatcgtca gccatggtga tgtttgagct ggcttggatg ctgtccaagg 700

acctgaatga catgctgtgg tgggccatcg ttggactaac agaccagtgg 750

gtgcaagaca agatcactca aatgaaatac gtgactgatg ttggtgtcct 800

gcagcgccac gtttcccgcc acaaccaccg gaacgaggat gaggagaaca 850

cactctccgt ggactgcaca cggatctcct ttgagtatga cctccgcctg 900

gtgctctacc agcactggtc cctccatgac agcctgtgca acaccagcta 950

taccgcagcc aggttcaagc tgtggtctgt gcatggacag aagcggctcc 1000

aggagttcct tgcagacatg ggtcttcccc tgaagcaggt gaagcagaag 1050

ttccaggcca tggacatctc cttgaaggag aatttgcggg aaatgattga 1100

agagtctgca aataaatttg ggatgaagga catgcgcgtg cagactttca 1150

gcattcattt tgggttcaag cacaagtttc tggccagcga cgtggtcttt 1200

gccaccatgt ctttgatgga gagccccgag aaggatggct cagggacaga 1250

tcacttcatc caggctctgg acagcctctc caggagtaac ctggacaagc 1300

tgtaccatgg cctggaactc gccaagaagc agctgcgagc cacccagcag 1350

accattgcca gctgc 1365

<210> 41
<211> 566
<212> PRT
<213> Homo sapiens

<400> 41

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Ser	Gln	Arg	Val	Leu	Leu	Phe	Val	Ala	Ser	Asp	Val	Asp	Ala	Leu	
				20				25						30	
Cys	Ala	Cys	Lys	Ile	Leu	Gln	Ala	Leu	Phe	Gln	Cys	Asp	His	Val	
				35				40						45	
Gln	Tyr	Thr	Leu	Val	Pro	Val	Ser	Gly	Trp	Gln	Glu	Leu	Glu	Thr	
				50				55						60	
Ala	Phe	Leu	Glu	His	Lys	Glu	Gln	Phe	His	Tyr	Phe	Ile	Leu	Ile	
				65				70						75	
Asn	Cys	Gly	Ala	Asn	Val	Asp	Leu	Leu	Asp	Ile	Leu	Gln	Pro	Asp	
				80				85						90	
Glu	Asp	Thr	Ile	Phe	Phe	Val	Cys	Asp	Ser	His	Arg	Pro	Val	Asn	
				95				100						105	
Val	Val	Asn	Val	Tyr	Asn	Asp	Thr	Gln	Ile	Lys	Leu	Leu	Ile	Lys	
				110				115						120	
Gln	Asp	Asp	Asp	Leu	Glu	Val	Pro	Ala	Tyr	Glu	Asp	Ile	Phe	Arg	
				125				130						135	
Asp	Glu	Glu	Glu	Asp	Glu	Glu	His	Ser	Gly	Asn	Asp	Ser	Asp	Gly	
				140				145						150	
Ser	Glu	Pro	Ser	Glu	Lys	Arg	Thr	Arg	Leu	Glu	Glu	Glu	Ile	Val	
				155				160						165	
Glu	Gln	Thr	Met	Arg	Arg	Arg	Gln	Arg	Arg	Glu	Trp	Glu	Ala	Arg	
				170				175						180	
Arg	Arg	Asp	Ile	Leu	Phe	Asp	Tyr	Glu	Gln	Tyr	Glu	Tyr	His	Gly	
				185				190						195	
Thr	Ser	Ser	Ala	Met	Val	Met	Phe	Glu	Leu	Ala	Trp	Met	Leu	Ser	
				200				205						210	
Lys	Asp	Leu	Asn	Asp	Met	Leu	Trp	Trp	Ala	Ile	Val	Gly	Leu	Thr	
				215				220						225	
Asp	Gln	Trp	Val	Gln	Asp	Lys	Ile	Thr	Gln	Met	Lys	Tyr	Val	Thr	
				230				235						240	
Asp	Val	Gly	Val	Leu	Gln	Arg	His	Val	Ser	Arg	His	Asn	His	Arg	

245 250 255

Asn Glu Asp Glu Glu Asn Thr Leu Ser Val Asp Cys Thr Arg Ile
260 265 270

Ser Phe Glu Tyr Asp Leu Arg Leu Val Leu Tyr Gln His Trp Ser
275 280 285

Leu His Asp Ser Leu Cys Asn Thr Ser Tyr Thr Ala Ala Arg Phe
290 295 300

Lys Leu Trp Ser Val His Gly Gln Lys Arg Leu Gln Glu Phe Leu
305 310 315

Ala Asp Met Gly Leu Pro Leu Lys Gln Val Lys Gln Lys Phe Gln
320 325 330

Ala Met Asp Ile Ser Leu Lys Glu Asn Leu Arg Glu Met Ile Glu
335 340 345

Glu Ser Ala Asn Lys Phe Gly Met Lys Asp Met Arg Val Gln Thr
350 355 360

Phe Ser Ile His Phe Gly Phe Lys His Lys Phe Leu Ala Ser Asp
365 370 375

Val Val Phe Ala Thr Met Ser Leu Met Glu Ser Pro Glu Lys Asp
380 385 390

Gly Ser Gly Thr Asp His Phe Ile Gln Ala Leu Asp Ser Leu Ser
395 400 405

Arg Ser Asn Leu Asp Lys Leu Tyr His Gly Leu Glu Leu Ala Lys
410 415 420

Lys Gln Leu Arg Ala Thr Gln Gln Thr Ile Ala Ser Cys Leu Cys
425 430 435

Thr Asn Leu Val Ile Ser Gln Gly Pro Phe Leu Tyr Cys Ser Leu
440 445 450

Met Glu Gly Thr Pro Asp Val Met Leu Phe Ser Arg Pro Ala Ser
455 460 465

Leu Ser Leu Leu Ser Lys His Leu Leu Lys Ser Phe Val Cys Ser
470 475 480

Thr Lys Asn Arg Arg Cys Lys Leu Leu Pro Leu Val Met Ala Ala
485 490 495

Pro Leu Ser Met Glu His Gly Thr Val Thr Val Val Gly Ile Pro
500 505 510

Pro Glu Thr Asp Ser Ser Asp Arg Lys Asn Phe Phe Gly Arg Ala
515 520 525

Phe Glu Lys Ala Ala Glu Ser Thr Ser Ser Arg Met Leu His Asn
530 535 540

His Phe Asp Leu Ser Val Ile Glu Leu Lys Ala Glu Asp Arg Ser
545 550 555

Lys Phe Leu Asp Ala Leu Ile Ser Leu Leu Ser

<210> 42
<211> 380
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 44, 118, 172, 183
<223> unknown base

<400> 42
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ccgatttccg caaagagttc tacgaggtgg tccagagcca gagggtcctt 100

ctcttcgtgg cctcggangt ggatgctctg tgtgcgtgca agatccttca 150

ggccttgttc cagtgtgacc angtgcaata tangctggtt ccagtttctg 200

ggtggcaaga acttgaaact gcatttcttg agcataaaga acagtttcat 250

tattttattc tcataaactg tggagctaat gtagacctat tggatattct 300

tcaacctgat gaagacacta tattctttgt gtgtgacacc cataggccag 350

tcaatgttgt caatgtatac aacgataccc 380

<210> 43
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
ttccgcaaag agttctacga ggtgg 25

<210> 44
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 44
attgacaaca ttgactggcc tatggg 26

<210> 45
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 45
gtggatgctc tgtgtgcgtg caagatcctt caggccttgt tccagtgtga 50

<210> 46

<211> 3089
<212> DNA
<213> Homo sapiens

<400> 46
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tttctagtga accacgaagg gacgatacca gaaaacaccc tcaacccaaa 100

ggaaatagac tacagcccca attggctgac tttggctata gaaaaaagaa 150

aggaacgaaa agagacagtt ttttttggaa agctaagtct tccctttatc 200

gagtcaagaa acccccccct cttgagctat ttacagcttt taacaattga 250

gtaaagtacg ctccggtcac catggtgaca gccgccctgg gtcccgtctg 300

ggcagcgctc ctgctctttc tcctgatgtg tgagatccgt atggtggagc 350

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agggtgacaa aggggaccca ggcccaatgg gcctgccagg gtacatgggc 550

agggagggtc cccaagggga gcctggccct cagggcagca agggtgacaa 600

gggggagatg ggcagccccg gcgccccgtg ccagaagcgc ttcttcgcct 650

tctcagtggg ccgcaagacg gccctgcaca gcggcgagga cttccagacg 700

ctgctcttcg aaagggtctt tgtgaacctt gatgggtgct ttgacatggc 750

gaccggccag tttgctgctc ccctgcgtgg catctacttc ttcagcctca 800

atgtgcacag ctggaattac aaggagacgt acgtgcacat tatgcataac 850

cagaaagagg ctgtcatcct gtacgcgcag cccagcgagc gcagcatcat 900

gcagagccag agtgtgatgc tggacctggc ctacggggac cgcgtctggg 950

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gacacctaca tcaccttcag cggccacctc atcaaggccg aggacgactg 1050

agggcctctg ggccaccctc ccggctggag agctcaggtg ctggtcccgt 1100

cccctgcagg gctcagtttg cactgctgtg aagcaggaag gccagggagg 1150

tccccgggga cctggcattc tggggagacc ctgcttctat cttggctgcc 1200

atcatccctc ccagcctatt tctgctcctc tcttctctct tggacctatt 1250

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PCT/US2003/030000

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Pro His Ala Leu Pro Glu Ile Arg Pro Tyr Ile Asn Ile Thr Ile
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Leu Lys Gly Asp Lys Gly Asp Pro Gly Pro Met Gly Leu Pro Gly
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Tyr Met Gly Arg Glu Gly Pro Gln Gly Glu Pro Gly Pro Gln Gly
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Ser Lys Gly Asp Lys Gly Glu Met Gly Ser Pro Gly Ala Pro Cys
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Gln Lys Arg Phe Phe Ala Phe Ser Val Gly Arg Lys Thr Ala Leu
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His Ser Gly Glu Asp Phe Gln Thr Leu Leu Phe Glu Arg Val Phe
            140                 145                 150

Val Asn Leu Asp Gly Cys Phe Asp Met Ala Thr Gly Gln Phe Ala
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Ala Pro Leu Arg Gly Ile Tyr Phe Phe Ser Leu Asn Val His Ser
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Trp Asn Tyr Lys Glu Thr Tyr Val His Ile Met His Asn Gln Lys
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Glu Ala Val Ile Leu Tyr Ala Gln Pro Ser Glu Arg Ser Ile Met
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Gln Ser Gln Ser Val Met Leu Asp Leu Ala Tyr Gly Asp Arg Val
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<212> PRT
<213> Homo sapiens

<400> 52

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				20					25					30	
Ser	Gln	Pro	Gln	Thr	Val	Phe	Cys	Thr	Ala	Arg	Gln	Gly	Thr	Thr	
				35					40					45	
Val	Pro	Arg	Asp	Val	Pro	Pro	Asp	Thr	Val	Gly	Leu	Tyr	Val	Phe	
				50					55					60	
Glu	Asn	Gly	Ile	Thr	Met	Leu	Asp	Ala	Gly	Ser	Phe	Ala	Gly	Leu	
				65					70					75	
Pro	Gly	Leu	Gln	Leu	Leu	Asp	Leu	Ser	Gln	Asn	Gln	Ile	Ala	Ser	
				80					85					90	

Leu Pro Ser Gly Val Phe Gln Pro Leu Ala Asn Leu Ser Asn Leu

95 100 105

Asp Leu Thr Ala Asn Arg Leu His Glu Ile Thr Asn Glu Thr Phe
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Arg Gly Leu Arg Arg Leu Glu Arg Leu Tyr Leu Gly Lys Asn Arg
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Ile Arg His Ile Gln Pro Gly Ala Phe Asp Thr Leu Asp Arg Leu
140 145 150

Leu Glu Leu Lys Leu Gln Asp Asn Glu Leu Arg Ala Leu Pro Pro
155 160 165

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170 175 180

Leu Leu Ala Leu Glu Pro Gly Ile Leu Asp Thr Ala Asn Val Glu
185 190 195

Ala Leu Arg Leu Ala Gly Leu Gly Leu Gln Gln Leu Asp Glu Gly
200 205 210

Leu Phe Ser Arg Leu Arg Asn Leu His Asp Leu Asp Val Ser Asp
215 220 225

Asn Gln Leu Glu Arg Val Pro Pro Val Ile Arg Gly Leu Arg Gly
230 235 240

Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg Ile Ala Gln Leu
245 250 255

Arg Pro Glu Asp Leu Ala Gly Leu Ala Ala Leu Gln Glu Leu Asp
260 265 270

Val Ser Asn Leu Ser Leu Gln Ala Leu Pro Gly Asp Leu Ser Gly
275 280 285

Leu Phe Pro Arg Leu Arg Leu Leu Ala Ala Ala Arg Asn Pro Phe
290 295 300

Asn Cys Val Cys Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu
305 310 315

Ser His Val Thr Leu Ala Ser Pro Glu Glu Thr Arg Cys His Phe
320 325 330

Pro Pro Lys Asn Ala Gly Arg Leu Leu Leu Glu Leu Asp Tyr Ala
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Asp Phe Gly Cys Pro Ala Thr Thr Thr Thr Ala Thr Val Pro Thr
350 355 360

Thr Arg Pro Val Val Arg Glu Pro Thr Ala Leu Ser Ser Ser Leu
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Ala Pro Thr Trp Leu Ser Pro Thr Ala Pro Ala Thr Glu Ala Pro
380 385 390

Ser Pro Pro Ser Thr Ala Pro Pro Thr Val Gly Pro Val Pro Gln
395 400 405

Pro Gln Asp Cys Pro Pro Ser Thr Cys Leu Asn Gly Gly Thr Cys

410 415 420

His Leu Gly Thr Arg His His Leu Ala Cys Leu Cys Pro Glu Gly
425 430 435

Phe Thr Gly Leu Tyr Cys Glu Ser Gln Met Gly Gln Gly Thr Arg
440 445 450

Pro Ser Pro Thr Pro Val Thr Pro Arg Pro Pro Arg Ser Leu Thr
455 460 465

Leu Gly Ile Glu Pro Val Ser Pro Thr Ser Leu Arg Val Gly Leu
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Gln Arg Tyr Leu Gln Gly Ser Ser Val Gln Leu Arg Ser Leu Arg
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Leu Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg Leu Val Thr
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Leu Arg Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr Gln Leu
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Arg Pro Asn Ala Thr Tyr Ser Val Cys Val Met Pro Leu Gly Pro
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Gly Arg Val Pro Glu Gly Glu Glu Ala Cys Gly Glu Ala His Thr
545 550 555

Pro Pro Ala Val His Ser Asn His Ala Pro Val Thr Gln Ala Arg
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Glu Gly Asn Leu Pro Leu Leu Ile Ala Pro Ala Leu Ala Ala Val
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590 595 600

Arg Gly Arg Ala Met Ala Ala Ala Ala Gln Asp Lys Gly Gln Val
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Gly Pro Gly Ala Gly Pro Leu Glu Leu Glu Gly Val Lys Val Pro
620 625 630

Leu Glu Pro Gly Pro Lys Ala Thr Glu Gly Gly Gly Glu Ala Leu
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Leu	Thr	Pro	Ala	Thr	Thr	Thr	Leu	Asp	Leu	Ser	Tyr	Asn	Leu	Leu	
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Phe	Gln	Leu	Gln	Ser	Ser	Asp	Phe	His	Ser	Val	Ser	Lys	Leu	Arg	
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Val	Leu	Ile	Leu	Cys	His	Asn	Arg	Ile	Gln	Gln	Leu	Asp	Leu	Lys	
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95 100 105

Asn Arg Leu Lys Ser Val Thr Trp Tyr Leu Leu Ala Gly Leu Arg
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Tyr Leu Asp Leu Ser Phe Asn Asp Phe Asp Thr Met Pro Ile Cys
125 130 135

Glu Glu Ala Gly Asn Met Ser His Leu Glu Ile Leu Gly Leu Ser
140 145 150

Gly Ala Lys Ile Gln Lys Ser Asp Phe Gln Lys Ile Ala His Leu
155 160 165

His Leu Asn Thr Val Phe Leu Gly Phe Arg Thr Leu Pro His Tyr
170 175 180

Glu Glu Gly Ser Leu Pro Ile Leu Asn Thr Thr Lys Leu His Ile
185 190 195

Val Leu Pro Met Asp Thr Asn Phe Trp Val Leu Leu Arg Asp Gly
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Ile Lys Thr Ser Lys Ile Leu Glu Met Thr Asn Ile Asp Gly Lys
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Trp Asp Asp Leu Phe Leu Ile Leu Gln Phe Val Trp His Thr Ser
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Val Glu His Phe Gln Ile Arg Asn Val Thr Phe Gly Gly Lys Ala
275 280 285

Tyr Leu Asp His Asn Ser Phe Asp Tyr Ser Asn Thr Val Met Arg
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Thr Ile Lys Leu Glu His Val His Phe Arg Val Phe Tyr Ile Gln
305 310 315

Gln Asp Lys Ile Tyr Leu Leu Leu Thr Lys Met Asp Ile Glu Asn
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Leu Thr Ile Ser Asn Ala Gln Met Pro His Met Leu Phe Pro Asn
335 340 345

Tyr Pro Thr Lys Phe Gln Tyr Leu Asn Phe Ala Asn Asn Ile Leu
350 355 360

Thr Asp Glu Leu Phe Lys Arg Thr Ile Gln Leu Pro His Leu Lys
365 370 375

Thr Leu Ile Leu Asn Gly Asn Lys Leu Glu Thr Leu Ser Leu Val
380 385 390

Ser Cys Phe Ala Asn Asn Thr Pro Leu Glu His Leu Asp Leu Ser
395 400 405

Gln Asn Leu Leu Gln His Lys Asn Asp Glu Asn Cys Ser Trp Pro
410 415 420

Glu Thr Val Val Asn Met Asn Leu Ser Tyr Asn Lys Leu Ser Asp
425 430 435

Ser Val Phe Arg Cys Leu Pro Lys Ser Ile Gln Ile Leu Asp Leu
440 445 450

Asn Asn Asn Gln Ile Gln Thr Val Pro Lys Glu Thr Ile His Leu
455 460 465

Met Ala Leu Arg Glu Leu Asn Ile Ala Phe Asn Phe Leu Thr Asp
470 475 480

Leu Pro Gly Cys Ser His Phe Ser Arg Leu Ser Val Leu Asn Ile
485 490 495

Glu Met Asn Phe Ile Leu Ser Pro Ser Leu Asp Phe Val Gln Ser
500 505 510

Cys Gln Glu Val Lys Thr Leu Asn Ala Gly Arg Asn Pro Phe Arg
515 520 525

Cys Thr Cys Glu Leu Lys Asn Phe Ile Gln Leu Glu Thr Tyr Ser
530 535 540

Glu Val Met Met Val Gly Trp Ser Asp Ser Tyr Thr Cys Glu Tyr
545 550 555

Pro Leu Asn Leu Arg Gly Thr Arg Leu Lys Asp Val His Leu His
560 565 570

Glu Leu Ser Cys Asn Thr Ala Leu Leu Ile Val Thr Ile Val Val
575 580 585

Ile Met Leu Val Leu Gly Leu Ala Val Ala Phe Cys Cys Leu His
590 595 600

Phe Asp Leu Pro Trp Tyr Leu Arg Met Leu Gly Gln Cys Thr Gln
605 610 615

Thr Trp His Arg Val Arg Lys Thr Thr Gln Glu Gln Leu Lys Arg
620 625 630

Asn Val Arg Phe His Ala Phe Ile Ser Tyr Ser Glu His Asp Ser
635 640 645

Leu Trp Val Lys Asn Glu Leu Ile Pro Asn Leu Glu Lys Glu Asp
650 655 660

Gly Ser Ile Leu Ile Cys Leu Tyr Glu Ser Tyr Phe Asp Pro Gly
665 670 675

Lys Ser Ile Ser Glu Asn Ile Val Ser Phe Ile Glu Lys Ser Tyr
680 685 690

Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Asn Glu Trp
695 700 705

Cys His Tyr Glu Phe Tyr Phe Ala His His Asn Leu Phe His Glu
710 715 720

Asn Ser Asp His Ile Ile Leu Ile Leu Leu Glu Pro Ile Pro Phe
725 730 735

Tyr Cys Ile Pro Thr Arg Tyr His Lys Leu Lys Ala Leu Leu Glu
740 745 750

Lys Lys Ala Tyr Leu Glu Trp Pro Lys Asp Arg Arg Lys Cys Gly
755 760 765

Leu Phe Trp Ala Asn Leu Arg Ala Ala Ile Asn Val Asn Val Leu
770 775 780

Ala Thr Arg Glu Met Tyr Glu Leu Gln Thr Phe Thr Glu Leu Asn
785 790 795

Glu Glu Ser Arg Gly Ser Thr Ile Ser Leu Met Arg Thr Asp Cys
800 805 810

Leu

<210> 58
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<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 58
tcccaccagg tatcataaac tgaa 24

<210> 59
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<220>
<223> Synthetic oligonucleotide probe

<400> 59
ttatagacaa tctgttctca tcagaga 27

<210> 60
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<400> 60
aaaaagcata cttggaatgg cccaaggata ggtgtaaatg 40

<210> 61
<211> 3772
<212> DNA
<213> Homo sapiens

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ccccccctgcg cccgccccgc gcctctgcgc gcccctgtcc gccccggccc 150

agcccagccc agccccgcgg gccggtcaca cgcgcagcca gccggccgcc 200

tcccgcgccc aagcgcgccg ctctgctgtg ccctgcgccc ttgccccgcg 250

ccagcttctg cgcccgcagc ccgcccggcg cccccggtga ccgtgaccct 300

gccctgggcg cggggcggag caggcatgtc ccgcccgggg accgctaccc 350

cagcgctggc cctggtgctc ctggcagtga ccctggccgg ggtcggagcc 400

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ttatgagaac caagagctct gagaaggctg ccaacgatga tcacagtgtc 700

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atggcctggg ggcacatcga gggagactca acatccaggc gggcattaat 850

gaaaatgatt tttatgacgg agcgtggtgc gcgggaagaa atgacctcca 900

gcagtggatt gaagtggatg ctcggcgcct gaccagattc actggtgtca 950

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caacattgga aaaagccacc agggcctgaa gctgtatgct gtggagatct 1400

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gcgtcctaag agaatccacc ctctctggcc ctgggacatt gcaagctgct 3100

acaaataaat tctgtgttct tttgacaata gcgtcattgc caagtgcaca 3150

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aaaaaaaaaa aaaaaaaaaa aa 3772

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<212> PRT
<213> Homo sapiens

<400> 62

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			20					25						30	
Glu	Asp	Pro	Asp	Tyr	Tyr	Gly	Gln	Glu	Ile	Trp	Ser	Arg	Glu	Pro	
			35					40						45	
Tyr	Tyr	Ala	Arg	Pro	Glu	Pro	Glu	Leu	Glu	Thr	Phe	Ser	Pro	Pro	
			50					55						60	
Leu	Pro	Ala	Gly	Pro	Gly	Glu	Glu	Trp	Glu	Arg	Arg	Pro	Gln	Glu	
			65					70						75	
Pro	Arg	Pro	Pro	Lys	Arg	Ala	Thr	Lys	Pro	Lys	Lys	Ala	Pro	Lys	
			80					85						90	
Arg	Glu	Lys	Ser	Ala	Pro	Glu	Pro	Pro	Pro	Pro	Gly	Lys	His	Ser	
			95					100						105	
Asn	Lys	Lys	Val	Met	Arg	Thr	Lys	Ser	Ser	Glu	Lys	Ala	Ala	Asn	
			110					115						120	
Asp	Asp	His	Ser	Val	Arg	Val	Ala	Arg	Glu	Asp	Val	Arg	Glu	Ser	
			125					130						135	
Cys	Pro	Pro	Leu	Gly	Leu	Glu	Thr	Leu	Lys	Ile	Thr	Asp	Phe	Gln	
			140					145						150	
Leu	His	Ala	Ser	Thr	Val	Lys	Arg	Tyr	Gly	Leu	Gly	Ala	His	Arg	
			155					160						165	
Gly	Arg	Leu	Asn	Ile	Gln	Ala	Gly	Ile	Asn	Glu	Asn	Asp	Phe	Tyr	
			170					175						180	
Asp	Gly	Ala	Trp	Cys	Ala	Gly	Arg	Asn	Asp	Leu	Gln	Gln	Trp	Ile	

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                185                 190                 195

Glu Val Asp Ala Arg Arg Leu Thr Arg Phe Thr Gly Val Ile Thr
            200                 205                 210

Gln Gly Arg Asn Ser Leu Trp Leu Ser Asp Trp Val Thr Ser Tyr
            215                 220                 225

Lys Val Met Val Ser Asn Asp Ser His Thr Trp Val Thr Val Lys
            230                 235                 240

Asn Gly Ser Gly Asp Met Ile Phe Glu Gly Asn Ser Glu Lys Glu
            245                 250                 255

Ile Pro Val Leu Asn Glu Leu Pro Val Pro Met Val Ala Arg Tyr
            260                 265                 270

Ile Arg Ile Asn Pro Gln Ser Trp Phe Asp Asn Gly Ser Ile Cys
            275                 280                 285

Met Arg Met Glu Ile Leu Gly Cys Pro Leu Pro Asp Pro Asn Asn
            290                 295                 300

Tyr Tyr His Arg Arg Asn Glu Met Thr Thr Thr Asp Asp Leu Asp
            305                 310                 315

Phe Lys His His Asn Tyr Lys Glu Met Arg Gln Leu Met Lys Val
            320                 325                 330

Val Asn Glu Met Cys Pro Asn Ile Thr Arg Ile Tyr Asn Ile Gly
            335                 340                 345

Lys Ser His Gln Gly Leu Lys Leu Tyr Ala Val Glu Ile Ser Asp
            350                 355                 360

His Pro Gly Glu His Glu Val Gly Glu Pro Glu Phe His Tyr Ile
            365                 370                 375

Ala Gly Ala His Gly Asn Glu Val Leu Gly Arg Glu Leu Leu Leu
            380                 385                 390

Leu Leu Val Gln Phe Val Cys Gln Glu Tyr Leu Ala Arg Asn Ala
            395                 400                 405

Arg Ile Val His Leu Val Glu Glu Thr Arg Ile His Val Leu Pro
            410                 415                 420

Ser Leu Asn Pro Asp Gly Tyr Glu Lys Ala Tyr Glu Gly Gly Ser
            425                 430                 435

Glu Leu Gly Gly Trp Ser Leu Gly Arg Trp Thr His Asp Gly Ile
            440                 445                 450

Asp Ile Asn Asn Asn Phe Pro Asp Leu Asn Thr Leu Leu Trp Glu
            455                 460                 465

Ala Glu Asp Arg Gln Asn Val Pro Arg Lys Val Pro Asn His Tyr
            470                 475                 480

Ile Ala Ile Pro Glu Trp Phe Leu Ser Glu Asn Ala Thr Val Ala
            485                 490                 495

Ala Glu Thr Arg Ala Val Ile Ala Trp Met Glu Lys Ile Pro Phe
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500 505 510

Val Leu Gly Gly Asn Leu Gln Gly Gly Glu Leu Val Val Ala Tyr
515 520 525

Pro Tyr Asp Leu Val Arg Ser Pro Trp Lys Thr Gln Glu His Thr
530 535 540

Pro Thr Pro Asp Asp His Val Phe Arg Trp Leu Ala Tyr Ser Tyr
545 550 555

Ala Ser Thr His Arg Leu Met Thr Asp Ala Arg Arg Arg Val Cys
560 565 570

His Thr Glu Asp Phe Gln Lys Glu Glu Gly Thr Val Asn Gly Ala
575 580 585

Ser Trp His Thr Val Ala Gly Ser Leu Asn Asp Phe Ser Tyr Leu
590 595 600

His Thr Asn Cys Phe Glu Leu Ser Ile Tyr Val Gly Cys Asp Lys
605 610 615

Tyr Pro His Glu Ser Gln Leu Pro Glu Glu Trp Glu Asn Asn Arg
620 625 630

Glu Ser Leu Ile Val Phe Met Glu Gln Val His Arg Gly Ile Lys
635 640 645

Gly Leu Val Arg Asp Ser His Gly Lys Gly Ile Pro Asn Ala Ile
650 655 660

Ile Ser Val Glu Gly Ile Asn His Asp Ile Arg Thr Ala Asn Asp
665 670 675

Gly Asp Tyr Trp Arg Leu Leu Asn Pro Gly Glu Tyr Val Val Thr
680 685 690

Ala Lys Ala Glu Gly Phe Thr Ala Ser Thr Lys Asn Cys Met Val
695 700 705

Gly Tyr Asp Met Gly Ala Thr Arg Cys Asp Phe Thr Leu Ser Lys
710 715 720

Thr Asn Met Ala Arg Ile Arg Glu Ile Met Glu Lys Phe Gly Lys
725 730 735

Gln Pro Val Ser Leu Pro Ala Arg Arg Leu Lys Leu Arg Gly Arg
740 745 750

Lys Arg Arg Gln Arg Gly
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<213> Artificial Sequence

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atccgcataa accctcagtc ctggtttgat aatgggagca tctgcatgag 50

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<212> DNA
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cccagccccg gcttcagctc tttcccaggt gttgactcca gctccagctt 150

cagctccagc tccaggtcgg gctccagctc cagccgcagc ttaggcagcg 200

gaggttctgt gtcccagttg ttttccaatt tcaccggctc cgtggatgac 250

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ggacagagtg gaacgcttgg aattcacagc tcatgttctt tctcagaagt 350

ttgagaaaga actttctaaa gtgagggaat atgtccaatt aattagtgtg 400

tatgaaaaga aactgttaaa cctaactgtc cgaattgaca tcatggagaa 450

ggataccatt tcttacactg aactggactt cgagctgatc aaggtagaag 500

tgaaggagat ggaaaaactg gtcatacagc tgaaggagag ttttggtgga 550

agctcagaaa ttgttgacca gctggaggtg gagataagaa atatgactct 600

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gccgagaaat cgtggctctg aagaccaagc tgaaagagtg tgaggcctct 700

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tccatgcctg gaagaaacct ggggacttag ttaggtagat taatatctgg 2000

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cctgcttttt cttttctctc attgtccacc ttactaaaag tcagtagaat 2250

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aaaa 2854

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				20					25						30
Ser	Pro	Gly	Phe	Ser	Ser	Phe	Pro	Gly	Val	Asp	Ser	Ser	Ser	Ser	
				35					40						45
Phe	Ser	Ser	Ser	Ser	Arg	Ser	Gly	Ser	Ser	Ser	Ser	Arg	Ser	Leu	
				50					55						60
Gly	Ser	Gly	Gly	Ser	Val	Ser	Gln	Leu	Phe	Ser	Asn	Phe	Thr	Gly	
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Ser	Val	Asp	Asp	Arg	Gly	Thr	Cys	Gln	Cys	Ser	Val	Ser	Leu	Pro	
				80					85						90
Asp	Thr	Thr	Phe	Pro	Val	Asp	Arg	Val	Glu	Arg	Leu	Glu	Phe	Thr	
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Ala	His	Val	Leu	Ser	Gln	Lys	Phe	Glu	Lys	Glu	Leu	Ser	Lys	Val	
				110					115						120
Arg	Glu	Tyr	Val	Gln	Leu	Ile	Ser	Val	Tyr	Glu	Lys	Lys	Leu	Leu	
				125					130						135
Asn	Leu	Thr	Val	Arg	Ile	Asp	Ile	Met	Glu	Lys	Asp	Thr	Ile	Ser	
				140					145						150
Tyr	Thr	Glu	Leu	Asp	Phe	Glu	Leu	Ile	Lys	Val	Glu	Val	Lys	Glu	
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Met	Glu	Lys	Leu	Val	Ile	Gln	Leu	Lys	Glu	Ser	Phe	Gly	Gly	Ser	
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Ser	Glu	Ile	Val	Asp	Gln	Leu	Glu	Val	Glu	Ile	Arg	Asn	Met	Thr	
				185					190						195
Leu	Leu	Val	Glu	Lys	Leu	Glu	Thr	Leu	Asp	Lys	Asn	Asn	Val	Leu	
				200					205						210

Ala Ile Arg Arg Glu Ile Val Ala Leu Lys Thr Lys Leu Lys Glu
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Cys Glu Ala Ser Lys Asp Gln Asn Thr Pro Val Val His Pro Pro
230 235 240

Pro Thr Pro Gly Ser Cys Gly His Gly Gly Val Val Asn Ile Ser
245 250 255

Lys Pro Ser Val Val Gln Leu Asn Trp Arg Gly Phe Ser Tyr Leu
260 265 270

Tyr Gly Ala Trp Gly Arg Asp Tyr Ser Pro Gln His Pro Asn Lys
275 280 285

Gly Leu Tyr Trp Val Ala Pro Leu Asn Thr Asp Gly Arg Leu Leu
290 295 300

Glu Tyr Tyr Arg Leu Tyr Asn Thr Leu Asp Asp Leu Leu Leu Tyr
305 310 315

Ile Asn Ala Arg Glu Leu Arg Ile Thr Tyr Gly Gln Gly Ser Gly
320 325 330

Thr Ala Val Tyr Asn Asn Asn Met Tyr Val Asn Met Tyr Asn Thr
335 340 345

Gly Asn Ile Ala Arg Val Asn Leu Thr Thr Asn Thr Ile Ala Val
350 355 360

Thr Gln Thr Leu Pro Asn Ala Ala Tyr Asn Asn Arg Phe Ser Tyr
365 370 375

Ala Asn Val Ala Trp Gln Asp Ile Asp Phe Ala Val Asp Glu Asn
380 385 390

Gly Leu Trp Val Ile Tyr Ser Thr Glu Ala Ser Thr Gly Asn Met
395 400 405

Val Ile Ser Lys Leu Asn Asp Thr Thr Leu Gln Val Leu Asn Thr
410 415 420

Trp Tyr Thr Lys Gln Tyr Lys Pro Ser Ala Ser Asn Ala Phe Met
425 430 435

Val Cys Gly Val Leu Tyr Ala Thr Arg Thr Met Asn Thr Arg Thr
440 445 450

Glu Glu Ile Phe Tyr Tyr Tyr Asp Thr Asn Thr Gly Lys Glu Gly
455 460 465

Lys Leu Asp Ile Val Met His Lys Met Gln Glu Lys Val Gln Ser
470 475 480

Ile Asn Tyr Asn Pro Phe Asp Gln Lys Leu Tyr Val Tyr Asn Asp
485 490 495

Gly Tyr Leu Leu Asn Tyr Asp Leu Ser Val Leu Gln Lys Pro Gln
500 505 510

<210> 68
<211> 410
<212> DNA

<213> Homo sapiens

<220>
<221> unsure
<222> 206, 217, 387
<223> unknown base

<400> 68
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cctgtcgtcc accctcctcc cactccaggg agctgtggtc atggtggtgt 100

ggtgaacatc agcaaaccgt ctgtggttca gctcaactgg agagggtttt 150

cttatctata tggtgcttgg ggtagggatt actctcccca gcatccaaac 200

aaaggnatgt attgggnggc gccattgaat acagatggga gactgttgga 250

gtattataga ctgtacaacc cactggatga tttgctattg tatataaatg 300

ctcgagagtt gcggatcacc tatggccaag gtagtggtac agcagtttac 350

aacaacaaca tgtacgtcaa catgtacaac accgggnata ttgccagagt 400

taacctgacc 410

<210> 69
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 69
agctgtggtc atggtggtgt ggtg 24

<210> 70
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 70
ctaccttggc cataggtgat ccgc 24

<210> 71
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 71
catcagcaaa ccgtctgtgg ttcagctcaa ctggagaggg tt 42

<210> 72
<211> 3127
<212> DNA
<213> Homo sapiens

<400> 72
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tcttgtctgt atccgctgct cttgtgacgt tgtggagatg gggagcgtcc 100

tggggctgtg ctccatggcg agctggatac catgtttgtg tggaagtgcc 150

ccgtgtttgc tatgccgatg ctgtcctagt ggaaacaact ccactgtaac 200

tagattgatc tatgcacttt tcttgcttgt tggagtatgt gtagcttgtg 250

taatgttgat accaggaatg gaagaacaac tgaataagat tcctggattt 300

tgtgagaatg agaaaggtgt tgtcccttgt aacattttgg ttggctataa 350

agctgtatat cgtttgtgct ttggtttggc tatgttctat cttcttctct 400

ctttactaat gatcaaagtg aagagtagca gtgatcctag agctgcagtg 450

cacaatggat tttggttctt taaatttgct gcagcaattg caattattat 500

tggggcattc ttcattccag aaggaacttt tacaactgtg tggttttatg 550

taggcatggc aggtgccttt tgtttcatcc tcatacaact agtcttactt 600

attgattttg cacattcatg gaatgaatcg tgggttgaaa aaatggaaga 650

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ctattttaaa attatattag accttaagct gttttagcaa gcattaaagc 1800

aaatgtatgg ctgccttttg aaatatttga tgtgttgcct ggcaggatac 1850

tgcaaagaac atggtttatt ttaaaattta taaacaagtc acttaaatgc 1900

cagttgtctg aaaaatctta taaggtttta cccttgatac ggaatttaca 1950

caggtaggga gtgtttagtg gacaatagtg taggttatgg atggaggtgt 2000

cggtactaaa ttgaataacg agtaaataat cttacttggg tagagatggc 2050

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ggttcagtgg aaatgtttgg aactctgaag gatttagaca aggttttgaa 2150

aaggataatc atgggttaga aggaagtgtt ttgaaagtca ctttgaaagt 2200

tagttttggg cccagcacgg tagctcaccc ttggtaatcc cagcactttg 2250

ggagcttaag tgggtagatt acttgagccc aggaattcag accagcttgg 2300

cacatggtga acctgttcta taaaaataat ctggctttga gcatatgcct 2350

gtggtccagc actgagaggc tagtgaagat tgctgagccc agagccaaag 2400

gttgcagtga gcaagtcacg tcactgcact ctagctggca cagagtaagc 2450

caaaaaaata tatatatatt gaaatcaagg aggcaaaatt ttgacaggga 2500

aggaagtaac tgcaaaacca ctaggcttta gtaggtactt atataaaatc 2550

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aatagctcag atagctaatt aggaaatttc aagttggcca ataatagcat 2650

tctctctgac atttaaaaat aatttctatt caaaatacat gcatattgat 2700

ttacacctca tactgtgata attaatgtga tgtggattgc tggtgtccag 2750

catgacccat aaacaggtca gaagaatgat ggaatgtttt agaataaact 2800

cctgcttata gtatactaca cagttcaaaa gatgtttaaa atgcttttgt 2850

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taatgaagct tttaaaatct acaatttctt ctttaaaaat atttattaat 3000

gtgaatggaa tataacaatt cagcttaatt ccccaacctt attctgtgtg 3050

tagacattgt attccacaat tttgaatggc tgtgttttac ctctaaataa 3100

atgaattcag agaaaaaaaa aaaaaaa 3127

<210> 73
<211> 453
<212> PRT
<213> Homo sapiens

<400> 73

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Met Gly Ser Val Leu Gly Leu Cys Ser Met Ala Ser Trp Ile Pro
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             20                  25                  30

Ser Gly Asn Asn Ser Thr Val Thr Arg Leu Ile Tyr Ala Leu Phe
         35                  40                  45

Leu Leu Val Gly Val Cys Val Ala Cys Val Met Leu Ile Pro Gly
     50                  55                  60

Met Glu Glu Gln Leu Asn Lys Ile Pro Gly Phe Cys Glu Asn Glu
 65                  70                  75

Lys Gly Val Val Pro Cys Asn Ile Leu Val Gly Tyr Lys Ala Val
             80                  85                  90

Tyr Arg Leu Cys Phe Gly Leu Ala Met Phe Tyr Leu Leu Leu Ser
         95                 100                 105

Leu Leu Met Ile Lys Val Lys Ser Ser Ser Asp Pro Arg Ala Ala
    110                 115                 120

Val His Asn Gly Phe Trp Phe Phe Lys Phe Ala Ala Ala Ile Ala
    125                 130                 135

Ile Ile Ile Gly Ala Phe Phe Ile Pro Glu Gly Thr Phe Thr Thr
    140                 145                 150

Val Trp Phe Tyr Val Gly Met Ala Gly Ala Phe Cys Phe Ile Leu
    155                 160                 165

Ile Gln Leu Val Leu Leu Ile Asp Phe Ala His Ser Trp Asn Glu
    170                 175                 180

Ser Trp Val Glu Lys Met Glu Glu Gly Asn Ser Arg Cys Trp Tyr
    185                 190                 195

Ala Ala Leu Leu Ser Ala Thr Ala Leu Asn Tyr Leu Leu Ser Leu
    200                 205                 210

Val Ala Ile Val Leu Phe Phe Val Tyr Tyr Thr His Pro Ala Ser
    215                 220                 225

Cys Ser Glu Asn Lys Ala Phe Ile Ser Val Asn Met Leu Leu Cys
    230                 235                 240

Val Gly Ala Ser Val Met Ser Ile Leu Pro Lys Ile Gln Glu Ser
    245                 250                 255

Gln Pro Arg Ser Gly Leu Leu Gln Ser Ser Val Ile Thr Val Tyr
    260                 265                 270

Thr Met Tyr Leu Thr Trp Ser Ala Met Thr Asn Glu Pro Glu Thr
    275                 280                 285
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Asn Cys Asn Pro Ser Leu Leu Ser Ile Ile Gly Tyr Asn Thr Thr
290 295 300

Ser Thr Val Pro Lys Glu Gly Gln Ser Val Gln Trp Trp His Ala
305 310 315

Gln Gly Ile Ile Gly Leu Ile Leu Phe Leu Leu Cys Val Phe Tyr
320 325 330

Ser Ser Ile Arg Thr Ser Asn Asn Ser Gln Val Asn Lys Leu Thr
335 340 345

Leu Thr Ser Asp Glu Ser Thr Leu Ile Glu Asp Gly Gly Ala Arg
350 355 360

Ser Asp Gly Ser Leu Glu Asp Gly Asp Asp Val His Arg Ala Val
365 370 375

Asp Asn Glu Arg Asp Gly Val Thr Tyr Ser Tyr Ser Phe Phe His
380 385 390

Phe Met Leu Phe Leu Ala Ser Leu Tyr Ile Met Met Thr Leu Thr
395 400 405

Asn Trp Ser Arg Tyr Glu Pro Ser Arg Glu Met Lys Ser Gln Trp
410 415 420

Thr Ala Val Trp Val Lys Ile Ser Ser Ser Trp Ile Gly Ile Val
425 430 435

Leu Tyr Val Trp Thr Leu Val Ala Pro Leu Val Leu Thr Asn Arg
440 445 450

Asp Phe Asp

<210> 74
<211> 480
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 48, 163
<223> unknown base

<400> 74
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cgttgtggag atggggagcg tccctggggc tgtgctccat ggcgagctgg 100

ataccatgtt tgtgtggaag tgccccgtgt ttgctatgcc gatgctgtcc 150

tagtggaaac aantccactg taactagatt gatctatgca cttttcttgc 200

ttgttggagt atgtgtagct tgtgtaatgt tgataccagg aatggaagaa 250

caactgaata agattcctgg attttgtgag aatgagaaag gtgttgtccc 300

ttgtaacatt ttggttggct ataaagctgt atatcgtttg tgctttggtt 350

tggctatgtt ctatcttctt ctctctttac taatgatcaa agtgaagagt 400

agcagtgatc ctagagctgc agtgcacaat ggattttggt tctttaaatt 450

tgctgcagca attgcaatta ttattggggc 480

<210> 75
<211> 438
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 32, 65, 92, 121, 142, 154, 170, 293, 315, 323
<223> unknown base

<400> 75
gttattgtga actttgtgga gatgggaggt cntggggctg tgttccatgg 50

cgagctggat accangtttg tgtggaagtg ccccgtgttt gntatgccga 100

tgctgtccta gtggaaacaa ntccactgta attagattga tntatgcact 150

tttnttgctt gttggagtan gtgtagcttg tgtaatgttg ataccaggaa 200

tggaagaaca actgaataag attcctggat tttgtgagaa tgagaaaggt 250

gttgtccctt gtaacatttt ggttggctat aaagctgtat atngtttgtg 300

ctttggtttg gctangttct atnttcttct ctctttacta atgatcaaag 350

tgaagagtag cagtgatcct agagctgcag tgcacaatgg attttggttt 400

tttaaatttg ctgcagcaat tgcaattatt attggggc 438

<210> 76
<211> 473
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 48
<223> unknown base

<400> 76
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gagatgggga gcgtccttgg ggttgtgctc catggcgagc tggataccat 100

gtttgtgtgg aagtgccccg tgtttgctat gccgatgctg tcctagtgga 150

aacaactcca ctgtaactag attgatctat gcacttttct tgcttgttgg 200

agtatgtgta gcttgtgtaa tgttgatacc aggaatggaa gaacaactga 250

ataagattcc tggattttgt gagaatgaga aaggtgttgt cccttgtaac 300

attttggttg gctataaagc tgtatatcgt ttgtgctttg gtttggctat 350

gttctatctt cttctctctt tactaatgat caaagtgaag agtagcagtg 400

atcctagagc tgcagtgcac aatggatttt ggttctttaa atttgctgca 450

gcaattgcaa ttattattgg ggc 473

<210> 77
<211> 666
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 21, 111
<223> unknown base

<400> 77
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acttttcct tgcttgttgg agtatgtgta gctttgtgta atgttgttcc 100

caggattgga ngaacaactg aataagattc ctggattttt gtgagaatga 150

gaaaggtgtt gtccccttgt aacatttttg gttggctata aagctgtata 200

tcgtttgtgc tttggtttgg ctatgttcta tcttcttctc tctttactaa 250

tgatcaaagt gaagagtagc agtgatccta gagctgcagt gcacaatgga 300

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cttcattcca gaaggaactt ttacaactgt gtggttttat gtaggcatgg 400

caggtgcctt ttgtttcatc ctcatacaac tagtcttact tattgatttt 450

gcacattcat ggaatgaatc gtgggttgaa aaaatggaag aagggaactc 500

gagatgttgg tatgcagcct tgttatcagc tacagctctg aattatctgc 550

tgtctttagt tgctatcgtc ctgttctttg tctactacac tcatccagcc 600

agttgttcag aaaacaaggc gttcatcagt gtcaacatgc tcctctgcgt 650

tggtgcttct gtaatg 666

<210> 78
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 78
atgtttgtgt ggaagtgccc cg 22

<210> 79
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 79
gtcaacatgc tcctctgc 18

<210> 80
<211> 26

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 80
aatccattgt gcactgcagc tctagg 26

<210> 81
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
gagcatgcca ccactggact gac 23

<210> 82
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 82
gccgatgctg tcctagtgga aacaactcca ctgtaactag attgatctat 50

gcac 54

<210> 83
<211> 3906
<212> DNA
<213> Homo sapiens

<400> 83
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ctgtgaaagc agataaaaga aaacatttat taacgtgtca ttacgagggg 200

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tgctgagtac cagacggcgt gtgagcagct gggacagaag tggcagtgtg 2000

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gggaaggtta agaaacaaca gaggtggacc tccaaaaaca tagaggcatc 3250

acctgactgc acaggcaatg aaaaaccatg tgggtgattt ccagcagacc 3300

tgtgctattg gccaggaggc ctgagaaagc aagcacgcac tctcagtcaa 3350

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ctcacaaagg aaaacggaga gagcgagcga gagagatttc cttggaaatt 3550

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tttacatgta atcaacatgg gaacttttag gggaacctaa taagaaatcc 3850

caattttcag gagtggtggt gtcaataaac gctctgtggc cagtgtaaaa 3900

gaaaaa 3906

<210> 84
<211> 867
<212> PRT
<213> Homo sapiens

<400> 84

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Phe Ser Leu Leu Gly Gly Ser Ser Ala Phe Leu Ser His His Arg
             20                  25                  30

Leu Lys Gly Arg Phe Gln Arg Asp Arg Arg Asn Ile Arg Pro Asn
             35                  40                  45

Ile Ile Leu Val Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser
             50                  55                  60

Met Gln Val Met Asn Lys Thr Arg Arg Ile Met Glu Gln Gly Gly
             65                  70                  75

Ala His Phe Ile Asn Ala Phe Val Thr Thr Pro Met Cys Cys Pro
             80                  85                  90

Ser Arg Ser Ser Ile Leu Thr Gly Lys Tyr Val His Asn His Asn
             95                 100                 105

Thr Tyr Thr Asn Asn Glu Asn Cys Ser Ser Pro Ser Trp Gln Ala
            110                 115                 120

Gln His Glu Ser Arg Thr Phe Ala Val Tyr Leu Asn Ser Thr Gly
            125                 130                 135

Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu Asn Glu Tyr Asn Gly
            140                 145                 150

Ser Tyr Val Pro Pro Gly Trp Lys Glu Trp Val Gly Leu Leu Lys
            155                 160                 165

Asn Ser Arg Phe Tyr Asn Tyr Thr Leu Cys Arg Asn Gly Val Lys
            170                 175                 180

Glu Lys His Gly Ser Asp Tyr Ser Lys Asp Tyr Leu Thr Asp Leu
            185                 190                 195

Ile Thr Asn Asp Ser Val Ser Phe Phe Arg Thr Ser Lys Lys Met
            200                 205                 210

Tyr Pro His Arg Pro Val Leu Met Val Ile Ser His Ala Ala Pro
            215                 220                 225

His Gly Pro Glu Asp Ser Ala Pro Gln Tyr Ser Arg Leu Phe Pro
            230                 235                 240

Asn Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn
            245                 250                 255
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Pro Asp Lys His Trp Ile Met Arg Tyr Thr Gly Pro Met Lys Pro
260 265 270

Ile His Met Glu Phe Thr Asn Met Leu Gln Arg Lys Arg Leu Gln
275 280 285

Thr Leu Met Ser Val Asp Asp Ser Met Glu Thr Ile Tyr Asn Met
290 295 300

Leu Val Glu Thr Gly Glu Leu Asp Asn Thr Tyr Ile Val Tyr Thr
305 310 315

Ala Asp His Gly Tyr His Ile Gly Gln Phe Gly Leu Val Lys Gly
320 325 330

Lys Ser Met Pro Tyr Glu Phe Asp Ile Arg Val Pro Phe Tyr Val
335 340 345

Arg Gly Pro Asn Val Glu Ala Gly Cys Leu Asn Pro His Ile Val
350 355 360

Leu Asn Ile Asp Leu Ala Pro Thr Ile Leu Asp Ile Ala Gly Leu
365 370 375

Asp Ile Pro Ala Asp Met Asp Gly Lys Ser Ile Leu Lys Leu Leu
380 385 390

Asp Thr Glu Arg Pro Val Asn Arg Phe His Leu Lys Lys Lys Met
395 400 405

Arg Val Trp Arg Asp Ser Phe Leu Val Glu Arg Gly Lys Leu Leu
410 415 420

His Lys Arg Asp Asn Asp Lys Val Asp Ala Gln Glu Glu Asn Phe
425 430 435

Leu Pro Lys Tyr Gln Arg Val Lys Asp Leu Cys Gln Arg Ala Glu
440 445 450

Tyr Gln Thr Ala Cys Glu Gln Leu Gly Gln Lys Trp Gln Cys Val
455 460 465

Glu Asp Ala Thr Gly Lys Leu Lys Leu His Lys Cys Lys Gly Pro
470 475 480

Met Arg Leu Gly Gly Ser Arg Ala Leu Ser Asn Leu Val Pro Lys
485 490 495

Tyr Tyr Gly Gln Gly Ser Glu Ala Cys Thr Cys Asp Ser Gly Asp
500 505 510

Tyr Lys Leu Ser Leu Ala Gly Arg Arg Lys Lys Leu Phe Lys Lys
515 520 525

Lys Tyr Lys Ala Ser Tyr Val Arg Ser Arg Ser Ile Arg Ser Val
530 535 540

Ala Ile Glu Val Asp Gly Arg Val Tyr His Val Gly Leu Gly Asp
545 550 555

Ala Ala Gln Pro Arg Asn Leu Thr Lys Arg His Trp Pro Gly Ala
560 565 570

Pro Glu Asp Gln Asp Asp Lys Asp Gly Gly Asp Phe Ser Gly Thr
575 580 585

Gly Gly Leu Pro Asp Tyr Ser Ala Ala Asn Pro Ile Lys Val Thr
590 595 600

His Arg Cys Tyr Ile Leu Glu Asn Asp Thr Val Gln Cys Asp Leu
605 610 615

Asp Leu Tyr Lys Ser Leu Gln Ala Trp Lys Asp His Lys Leu His
620 625 630

Ile Asp His Glu Ile Glu Thr Leu Gln Asn Lys Ile Lys Asn Leu
635 640 645

Arg Glu Val Arg Gly His Leu Lys Lys Lys Arg Pro Glu Glu Cys
650 655 660

Asp Cys His Lys Ile Ser Tyr His Thr Gln His Lys Gly Arg Leu
665 670 675

Lys His Arg Gly Ser Ser Leu His Pro Phe Arg Lys Gly Leu Gln
680 685 690

Glu Lys Asp Lys Val Trp Leu Leu Arg Glu Gln Lys Arg Lys Lys
695 700 705

Lys Leu Arg Lys Leu Leu Lys Arg Leu Gln Asn Asn Asp Thr Cys
710 715 720

Ser Met Pro Gly Leu Thr Cys Phe Thr His Asp Asn Gln His Trp
725 730 735

Gln Thr Ala Pro Phe Trp Thr Leu Gly Pro Phe Cys Ala Cys Thr
740 745 750

Ser Ala Asn Asn Asn Thr Tyr Trp Cys Met Arg Thr Ile Asn Glu
755 760 765

Thr His Asn Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu
770 775 780

Tyr Phe Asp Leu Asn Thr Asp Pro Tyr Gln Leu Met Asn Ala Val
785 790 795

Asn Thr Leu Asp Arg Asp Val Leu Asn Gln Leu His Val Gln Leu
800 805 810

Met Glu Leu Arg Ser Cys Lys Gly Tyr Lys Gln Cys Asn Pro Arg
815 820 825

Thr Arg Asn Met Asp Leu Asp Gly Gly Ser Tyr Glu Gln Tyr Arg
830 835 840

Gln Phe Gln Arg Arg Lys Trp Pro Glu Met Lys Arg Pro Ser Ser
845 850 855

Lys Ser Leu Gly Gln Leu Trp Glu Gly Trp Glu Gly
860 865

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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 85
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<210> 86
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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<400> 86
ggccagctat ctccgcag 18

<210> 87
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<220>
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<400> 87
aagggcctgc aagagaag 18

<210> 88
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<220>
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<400> 88
cactgggaca actgtggg 18

<210> 89
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<220>
<223> Synthetic oligonucleotide probe

<400> 89
cagaggcaac gtggagag 18

<210> 90
<211> 21
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 90
aagtattgtc atacagtgtt c 21

<210> 91
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 91
tagtacttgg gcacgaggtt ggag 24

<210> 92
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 92
tcataccaac tgctggtcat tggc 24

<210> 93
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 93
ctcaagctgc tggacacgga gcggccggtg aatcggtttc acttg 45

<210> 94
<211> 971
<212> DNA
<213> Homo sapiens

<400> 94
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aaggagtgag gagctgctgg gcagagaggg actgtccggc tcccagatgc 100

tgggcctcct ggggagcaca gccctcgtgg gatggatcac aggtgctgct 150

gtggcggtcc tgctgctgct gctgctgctg gccacctgcc ttttccacgg 200

acggcaggac tgtgacgtgg agaggaaccg tacagctgca gggggaaacc 250

gagtccgccg ggcccagcct tggcccttcc ggcggcgggg ccacctggga 300

atctttcacc atcaccgtca tcctggccac gtatctcatg tgccgaatgt 350

gggcctccac caccaccacc acccccgcca cacccctcac cacctccacc 400

accaccacca cccccaccgc caccatcccc gccacgctcg ctgaggctgc 450

tgtcgccggt gcctgtggac agcagctgcc cctgccctcc catctgttcc 500

caggacaagt ggaccccatg tttccatgtg gaaggatgca tctctggggt 550

gaacgagggg aacaatagac tggggcttgc tccagctgca tttgcatggc 600

atgccccagt gtactatggc agcagagaat ggaggaacac tgggtctgca 650

gtgctgaagg gtttggggag tggagagcaa gggtgctctt tcggggctgg 700

acagcccgtc ttgtgacagt gactcccagt gagccccaga aatgacaagc 750

gtgtcttggc agagccagca cacaagtgga tgtgaagtgc ccgtcttgac 800

ctcctcatca ggctgctgca ggcctctggc gggcagggca ctgggagagg 850

ccctgagaat gtccttttgg tttggagaag gcagtgtgag gctgcacagt 900

caattcatcg gtgccttagt ccaagaaaat aaaaaccact aagaagcttt 950

aaaaaaaaaa aaaaaaaaaa a 971

<210> 95
<211> 115
<212> PRT
<213> Homo sapiens

<400> 95

Met	Leu	Gly	Leu	Leu	Gly	Ser	Thr	Ala	Leu	Val	Gly	Trp	Ile	Thr	
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Gly	Ala	Ala	Val	Ala	Val	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Thr	
			20					25						30	
Cys	Leu	Phe	His	Gly	Arg	Gln	Asp	Cys	Asp	Val	Glu	Arg	Asn	Arg	
			35					40						45	
Thr	Ala	Ala	Gly	Gly	Asn	Arg	Val	Arg	Arg	Ala	Gln	Pro	Trp	Pro	
			50					55						60	
Phe	Arg	Arg	Arg	Gly	His	Leu	Gly	Ile	Phe	His	His	His	Arg	His	
			65					70						75	
Pro	Gly	His	Val	Ser	His	Val	Pro	Asn	Val	Gly	Leu	His	His	His	
			80					85						90	
His	His	Pro	Arg	His	Thr	Pro	His	His	Leu	His	His	His	His	His	
			95					100						105	
Pro	His	Arg	His	His	Pro	Arg	His	Ala	Arg						
			110					115							

<210> 96
<211> 1312
<212> DNA
<213> Homo sapiens

<400> 96
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gctgacgctg ctggcctttg ccgggtactc agggctactg gctggggtgg 150

aagtgagtgc tgggtcaccc cccatccgca acgtcactgt ggcctacaag 200

ttccacatgg ggctctatgg tgagactggg cggcttttca ctgagagctg 250

cagcatctct cccaagctcc gctccatcgc tgtctactat gacaaccccc 300

acatggtgcc ccctgataag tgccgatgtg ccgtgggcag catcctgagt 350

gaaggtgagg aatcgccctc ccctgagctc atcgacctct accagaaatt 400

tggcttcaag gtgttctcct tcccggcacc cagccatgtg gtgacagcca 450

ccttccccta caccaccatt ctgtccatct ggctggctac ccgccgtgtc 500

catcctgcct tggacaccta catcaaggag cggaagctgt gtgcctatcc 550

tcggctggag atctaccagg aagaccagat ccatttcatg tgcccactgg 600

cacggcaggg agacttctat gtgcctgaga tgaaggagac agagtggaaa 650

tggcgggggc ttgtggaggc cattgacacc caggtggatg gcacaggagc 700

tgacacaatg agtgacacga gttctgtaag cttggaagtg agccctggca 750

gccgggagac ttcagctgcc acactgtcac ctggggcgag cagccgtggc 800

tgggatgacg gtgacacccg cagcgagcac agctacagcg agtcaggtgc 850

cagcggctcc tcttttgagg agctggactt ggagggcgag gggcccttag 900

gggagtcacg gctggaccct gggactgagc ccctggggac taccaagtgg 950

ctctgggagc ccactgcccc tgagaagggc aaggagtaac ccatggcctg 1000

caccctcctg cagtgcagtt gctgaggaac tgagcagact ctccagcaga 1050

ctctccagcc ctcttcctcc ttcctctggg ggaggagggg ttcctgaggg 1100

acctgacttc ccctgctcca ggcctcttgc taagccttct cctcactgcc 1150

ctttaggctc ccagggccag aggagccagg gactattttc tgcaccagcc 1200

cccagggctg ccgcccctgt tgtgtctttt tttcagactc acagtggagc 1250

ttccaggacc cagaataaag ccaatgattt acttgtttca cctggaaaaa 1300

aaaaaaaaaa aa 1312

<210> 97
<211> 313
<212> PRT
<213> Homo sapiens

<400> 97

Met	Ser	Asp	Leu	Leu	Leu	Leu	Gly	Leu	Ile	Gly	Gly	Leu	Thr	Leu	
1				5				10						15	
Leu	Leu	Leu	Leu	Thr	Leu	Leu	Ala	Phe	Ala	Gly	Tyr	Ser	Gly	Leu	
				20				25						30	
Leu	Ala	Gly	Val	Glu	Val	Ser	Ala	Gly	Ser	Pro	Pro	Ile	Arg	Asn	
				35				40						45	
Val	Thr	Val	Ala	Tyr	Lys	Phe	His	Met	Gly	Leu	Tyr	Gly	Glu	Thr	
				50				55						60	
Gly	Arg	Leu	Phe	Thr	Glu	Ser	Cys	Ser	Ile	Ser	Pro	Lys	Leu	Arg	
				65				70						75	

Ser Ile Ala Val Tyr Tyr Asp Asn Pro His Met Val Pro Pro Asp
80 85 90

Lys Cys Arg Cys Ala Val Gly Ser Ile Leu Ser Glu Gly Glu Glu
95 100 105

Ser Pro Ser Pro Glu Leu Ile Asp Leu Tyr Gln Lys Phe Gly Phe
110 115 120

Lys Val Phe Ser Phe Pro Ala Pro Ser His Val Val Thr Ala Thr
125 130 135

Phe Pro Tyr Thr Thr Ile Leu Ser Ile Trp Leu Ala Thr Arg Arg
140 145 150

Val His Pro Ala Leu Asp Thr Tyr Ile Lys Glu Arg Lys Leu Cys
155 160 165

Ala Tyr Pro Arg Leu Glu Ile Tyr Gln Glu Asp Gln Ile His Phe
170 175 180

Met Cys Pro Leu Ala Arg Gln Gly Asp Phe Tyr Val Pro Glu Met
185 190 195

Lys Glu Thr Glu Trp Lys Trp Arg Gly Leu Val Glu Ala Ile Asp
200 205 210

Thr Gln Val Asp Gly Thr Gly Ala Asp Thr Met Ser Asp Thr Ser
215 220 225

Ser Val Ser Leu Glu Val Ser Pro Gly Ser Arg Glu Thr Ser Ala
230 235 240

Ala Thr Leu Ser Pro Gly Ala Ser Ser Arg Gly Trp Asp Asp Gly
245 250 255

Asp Thr Arg Ser Glu His Ser Tyr Ser Glu Ser Gly Ala Ser Gly
260 265 270

Ser Ser Phe Glu Glu Leu Asp Leu Glu Gly Glu Gly Pro Leu Gly
275 280 285

Glu Ser Arg Leu Asp Pro Gly Thr Glu Pro Leu Gly Thr Thr Lys
290 295 300

Trp Leu Trp Glu Pro Thr Ala Pro Glu Lys Gly Lys Glu
305 310

<210> 98
<211> 725
<212> DNA
<213> Homo sapiens

<400> 98
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ctgaggctgg gctcgaaacc gaaagtcccg tccggaccct ccaagtggag 200

accctggtgg agcccccaga accatgtgcc gagcccgctg cttttggaga 250

cacgcttcac atacactaca cgggaagctt ggtagatgga cgtattattg 300

acacctccct gaccagagac cctctggtta tagaacttgg ccaaaagcag 350

gtgattccag gtctggagca gagtcttctc gacatgtgtg tgggagagaa 400

gcgaagggca atcattcctt ctcacttggc ctatggaaaa cggggatttc 450

caccatctgt cccagcggat gcagtggtgc agtatgacgt ggagctgatt 500

gcactaatcc gagccaacta ctggctaaag ctggtgaagg gcattttgcc 550

tctggtaggg atggccatgg tgccagccct cctgggcctc attgggtatc 600

acctatacag aaaggccaat agacccaaag tctccaaaaa gaagctcaag 650

gaagagaaac gaaacaagag caaaaagaaa taataaataa taaattttaa 700

aaaacttaaa aaaaaaaaaa aaaaa 725

<210> 99
<211> 201
<212> PRT
<213> Homo sapiens

<400> 99

Met	Thr	Leu	Arg	Pro	Ser	Leu	Leu	Pro	Leu	His	Leu	Leu	Leu	Leu	
1				5				10						15	
Leu	Leu	Leu	Ser	Ala	Ala	Val	Cys	Arg	Ala	Glu	Ala	Gly	Leu	Glu	
			20					25						30	
Thr	Glu	Ser	Pro	Val	Arg	Thr	Leu	Gln	Val	Glu	Thr	Leu	Val	Glu	
			35					40						45	
Pro	Pro	Glu	Pro	Cys	Ala	Glu	Pro	Ala	Ala	Phe	Gly	Asp	Thr	Leu	
			50					55						60	
His	Ile	His	Tyr	Thr	Gly	Ser	Leu	Val	Asp	Gly	Arg	Ile	Ile	Asp	
			65					70						75	
Thr	Ser	Leu	Thr	Arg	Asp	Pro	Leu	Val	Ile	Glu	Leu	Gly	Gln	Lys	
			80					85						90	
Gln	Val	Ile	Pro	Gly	Leu	Glu	Gln	Ser	Leu	Leu	Asp	Met	Cys	Val	
			95					100						105	
Gly	Glu	Lys	Arg	Arg	Ala	Ile	Ile	Pro	Ser	His	Leu	Ala	Tyr	Gly	
			110					115						120	
Lys	Arg	Gly	Phe	Pro	Pro	Ser	Val	Pro	Ala	Asp	Ala	Val	Val	Gln	
			125					130						135	
Tyr	Asp	Val	Glu	Leu	Ile	Ala	Leu	Ile	Arg	Ala	Asn	Tyr	Trp	Leu	
			140					145						150	
Lys	Leu	Val	Lys	Gly	Ile	Leu	Pro	Leu	Val	Gly	Met	Ala	Met	Val	
			155					160						165	
Pro	Ala	Leu	Leu	Gly	Leu	Ile	Gly	Tyr	His	Leu	Tyr	Arg	Lys	Ala	
			170					175						180	
Asn	Arg	Pro	Lys	Val	Ser	Lys	Lys	Lys	Leu	Lys	Glu	Glu	Lys	Arg	

185 190 195

Asn Lys Ser Lys Lys Lys
200

<210> 100
<211> 705
<212> DNA
<213> Homo sapiens

<400> 100
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cgctccatct gctgctgctg ctgctgctca gtgcggcggt gtgccgggct 150

gaggctgggc tcgaaaccga aagtcccgtc cggaccctcc aagtggagac 200

cctggtggag cccccagaac catgtgccga gcccgctgct tttggagaca 250

cgcttcacat acactacacg ggaagcttgg tagatggacg tattattgac 300

acctccctga ccagagaccc tctggttata gaacttggcc aaaagcaggt 350

gattccaggt ctggagcaga gtcttctcga catgtgtgtg ggagagaagc 400

gaagggcaat cattccttct cacttggcct atggaaaacg gggatttcca 450

ccatctgtcc cagcggatgc agtggtgcag tatgacgtgg agctgattgc 500

actaatccga gccaactact ggctaaagct ggtgaagggc attttgcctc 550

tggtagggat ggccatggtg ccaccctcct gggcctcatt gggtatcacc 600

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gagaaacgaa acaagagcaa aaagaaataa taaataataa attttaaaaa 700

actta 705

<210> 101
<211> 543
<212> DNA
<213> Homo sapiens

<400> 101
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gaaccatgtg ccgagcccgc tgcttttgga gacacgcttc acatacacta 100

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accctctggt tatagaactt ggccaaaagc aggtgattcc aggtctggag 200

cagagtcttc tcgacatgtg tgtgggagag aagcgaaggg caatcattcc 250

ttctcacttg gcctatggaa aacggggatt tccaccatct gtcccagcgg 300

atgcagtggt gcagtatgac gtggagctga ttgcactaat ccgagccaac 350

tactggctaa agctggtgaa gggcattttg cctctggtag ggatggccat 400

ggtgccagcc ctcctgggcc tcattgggta tcacctatac agaaaggcca 450

atagacccaa agtctccaaa aagaagctca aggaagagaa acgaaacaag 500

agcaaaaaga aataataaat aataaatttt aaaaaactta aaa 543

<210> 102
<211> 1316
<212> DNA
<213> Homo sapiens

<400> 102
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ccactgcacg acggggctgg actgacctga aaaaaatgtc tggatttcta 150

gagggcttga gatgctcaga atgcattgac tgggggggaaa agcgcaatac 200

tattgcttcc attgctgctg gtgtactatt ttttacaggc tggtggatta 250

tcatagatgc agctgttatt tatcccacca tgaaagattt caaccactca 300

taccatgcct gtggtgttat agcaaccata gccttcctaa tgattaatgc 350

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tcatcttttt tggagggctg gtttttaagt ttggccgcac tgaagactta 600

tggcagtgaa cacatctgat ttcccacagc acaacagccc tgcatgggtt 650

tgtttgtttt tttactgctc actcccaacc ttttgtaatg ccattttcta 700

aacttatttc tgagtgtagt ctcagcttaa agttgtgtaa tactaaaatc 750

acgagaacac ctaaacaaca accaaaaatc tattgtggta tgcacttgat 800

taacttataa aatgttagag gaaactttca catgaataat ttttgtcaaa 850

ttttatcatg gtataatttg taaaaataaa aagaaattac aaaagaaatt 900

atggatttgt caatgtaagt atttgtcata tctgaggtcc aaaaccacaa 950

tgaaagtgct ctgaagattt aatgtgttta ttcaaatgtg gtctcttctg 1000

tgtcaaatgt taaatgaaat ataaacattt tttagttttt aaaatattcc 1050

gtggtcaaaa ttcttcctca ctataattgg tatttacttt taccaaaaat 1100

tctgtgaaca tgtaatgtaa ctggcttttg agggtctccc aaggggtgag 1150

tggacgtgtt ggaagagaga agcaccatgg tccagccacc aggctccctg 1200

tgtcccttcc atgggaaggt cttccgctgt gcctctcatt ccaagggcag 1250

gaagatgtga ctcagccatg acacgtggtt ctggtgggat gcacagtcac 1300

tccacatcca ccactg 1316

<210> 103
<211> 157
<212> PRT
<213> Homo sapiens

<400> 103

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Trp	Gly	Glu	Lys	Arg	Asn	Thr	Ile	Ala	Ser	Ile	Ala	Ala	Gly	Val	
				20				25						30	
Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Ile	Ile	Asp	Ala	Ala	Val	Ile	
				35				40						45	
Tyr	Pro	Thr	Met	Lys	Asp	Phe	Asn	His	Ser	Tyr	His	Ala	Cys	Gly	
				50				55						60	
Val	Ile	Ala	Thr	Ile	Ala	Phe	Leu	Met	Ile	Asn	Ala	Val	Ser	Asn	
				65				70						75	
Gly	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Ser	Glu	Gly	Cys	Leu	Gly	Gln	
				80				85						90	
Thr	Gly	Ala	Arg	Ile	Trp	Leu	Phe	Val	Gly	Phe	Met	Leu	Ala	Phe	
				95				100						105	
Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Gly	Tyr	Val	
				110				115						120	
Ala	Lys	Glu	Lys	Asp	Ile	Val	Tyr	Pro	Gly	Ile	Ala	Val	Phe	Phe	
				125				130						135	
Gln	Asn	Ala	Phe	Ile	Phe	Phe	Gly	Gly	Leu	Val	Phe	Lys	Phe	Gly	
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Arg	Thr	Glu	Asp	Leu	Trp	Gln									
				155											

<210> 104
<211> 545
<212> DNA
<213> Homo sapiens

<400> 104
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tggatttcta gagggcttga gatgctcaga atgcattgac tgggggggaaa 150

agcgcaatac tattgcttcc attgctgctg gtgtactatt ttttacaggc 200

tggtggatta tcatagatgc agctgttatt tatcccacca tgaaagattt 250

caaccactca taccatgcct gtggtgttat agcaaccata gccttcctaa 300

tgattaatgc agtatcgaat ggacaagtcc gaggtgatag ttacagtgaa 350

ggttgtctgg gtcaaacagg tgctcgcatt tggcttttcg ttggtttcat 400

gttggccttt ggatctctga ttgcatctat gtggattctt tttggaggtt 450

atgttgctaa agaaaaagac atagtatacc ctggaattgc tgtatttttc 500

cagaatgcct tcatcttttt tggagggctg gtttttaagt ttggc 545

<210> 105
<211> 490
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 31, 39, 108, 145, 179, 219, 412, 479
<223> unknown base

<400> 105
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agaatgcatg actgggggaa aagcgcaaat actattgctt ccattgctgc 100

tggtgtanta ttttttacag gctggtggat tatcatagat gcagntgtta 150

tttatcccac catgaaagat ttcaaccant cataccatgc ctgtggtgtt 200

atagcaacca tagccttcnt aatgattaat gcagtatcga atggacaagt 250

ccgaggtgat agttacagtg aaggttgttt gggtcaaaca ggtgctcgca 300

tttggctttt cgttggtttc atgttggcct ttggatctct gattgcatct 350

atgtggattc tttttggagg ttatgttgct aaagaaaaag acatagtata 400

ccctggaatt gntgtatttt tccagaatgc cttcatcttt tttggagggc 450

tggtttttaa gtttggccgc actgaagant tatggcagtg 490

<210> 106
<211> 466
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 26, 38, 81, 115, 207, 329, 380, 446, 449
<223> unknown base

<400> 106
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aatgtttgga tttttagagg gcttgagatg ntcagaatgc attgactggg 100

ggaaaagcgc aatantattg ctttccattg ctgctggtgt actatttttt 150

acagggtggt ggattatcat agatgcagct gttatttatc ccaccatgaa 200

agatttnaac cactcatacc atgcctgtgg tgttatagca accatagcct 250

tcctaatgat taatgcagta tcgaatggac aagtccgagg tgatagttac 300

agtgaaggtt gtttgggtca aacaggtgnt cgcatttggc ttttcgttgg 350

tttcatgttg gcctttggat ttctgattgn attctatgcg gattcttctt 400

ggaggttatg ttgctaaaga aaaagacata gtataccctg gaattnctnt 450

atttttccag aatgcc 466

<210> 107
<211> 377
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 52, 67, 70, 78, 105, 144, 150, 209, 266, 268, 282, 310, 331, 356
<223> unknown base

<400> 107
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antattgctt ccattgntgn tggtgtanta ttttttttaca ggctggtgga 100

ttatnataga tgcagctgtt atttatccca ccatgaaaga tttnaaccan 150

tcataccatg cctgtggtgt tatagcaacc atagccttcc taatgattaa 200

tgcagtatng aatggacaag tccgaggtga tagttacagt gaaggttgtt 250

tgggtcaaac aggtgntngc atttggcttt tngttggttt catgttggcc 300

tttggatctn tgattgcatt tatgtggatt ntttttggag gttatgttgc 350

taaagnaaaa gacatagtat accctgt 377

<210> 108
<211> 552
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 12, 25, 65, 130, 437, 537
<223> unknown base

<400> 108
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ggactgacct gaaaaaaatg tttggatttn tagagggctt gagatgctca 150

gaatgcattg actgggggga aaagcgcaat actattgctt ccattgctgc 200

tggtgtacta ttttttacag gctggtggat tatcatagat gcagctgtta 250

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atagcaacca tagccttcct aatgattaat gcagtatcga atggacaagt 350

ccgaggtgat agttacagtg aaggttgtct gggtcaaaca ggtgctcgca 400

tttggctttt cgttggtttc atgttggcct ttggatntct gattgcatct 450

atgtggattc tttttggagg ttatgttgct aaagaaaaag acatagtata 500

ccctggaatt gctgtatttt tccagaatgc cttcatnttt tttggagggc 550

tg 552

<210> 109
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 109
gggtggatgg tactgctgca tcc 23

<210> 110
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 110
tgttgtgctg tgggaaatca gatgtg 26

<210> 111
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 111
gtgtctggag gctgtggccg ttttgttttc ttgggctaaa atcggg 46

<210> 112
<211> 3004
<212> DNA
<213> Homo sapiens

<400> 112
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ccgaatcctt tctccgaaga tgtcaaacgg cccccagcgc ccctggtaac 150

tgacaaggag gccaggaaga aggttctcaa acaagctttt tcagccaacc 200

aagtgccgga gaagctggat gtggtggtaa ttggcagtgg ctttgggggc 250

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ggaacaacat accaaggcag ggggctgctg tcataccttt ggaaagaatg 350

gccttgaatt tgacacagga atccattaca ttgggcgtat ggaagagggc 400

agcattggcc gttttatctt ggaccagatc actgaagggc agctggactg 450

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gccgaaagga gtaccccatg tacagtggag agaaagccta cattcagggc 550

ctcaaggaga agtttccaca ggaggaagct atcattgaca agtatataaa 600

gctggttaag gtggtatcca gtggagcccc tcatgccatc ctgttgaaat 650

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gcagcagctg ggggcctcct ctgagctcca ggcagtactc agctacatct 800

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cagtgaaatt gccttccaca ccatccctgt gattcagcgg gctgggggcg 950

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acacggacat ggaccaggcg atggagcgct acgtctccat gcccagggaa 1300

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cagttatgtc tttggtatca gacatacgaa aggtctcttt gtagttcgtg 2950

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aaaa 3004

<210> 113
<211> 610
<212> PRT
<213> Homo sapiens

<400> 113

Met Trp Leu Pro Leu Val Leu Leu Leu Ala Val Leu Leu Leu Ala
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Val Leu Cys Lys Val Tyr Leu Gly Leu Phe Ser Gly Ser Ser Pro
20 25 30

Asn Pro Phe Ser Glu Asp Val Lys Arg Pro Pro Ala Pro Leu Val
35 40 45

Thr Asp Lys Glu Ala Arg Lys Lys Val Leu Lys Gln Ala Phe Ser
50 55 60

Ala Asn Gln Val Pro Glu Lys Leu Asp Val Val Val Ile Gly Ser
65 70 75

Gly Phe Gly Gly Leu Ala Ala Ala Ala Ile Leu Ala Lys Ala Gly
80 85 90

Lys Arg Val Leu Val Leu Glu Gln His Thr Lys Ala Gly Gly Cys
95 100 105

Cys His Thr Phe Gly Lys Asn Gly Leu Glu Phe Asp Thr Gly Ile
110 115 120

His Tyr Ile Gly Arg Met Glu Glu Gly Ser Ile Gly Arg Phe Ile
125 130 135

Leu Asp Gln Ile Thr Glu Gly Gln Leu Asp Trp Ala Pro Leu Ser
140 145 150

Ser Pro Phe Asp Ile Met Val Leu Glu Gly Pro Asn Gly Arg Lys
155 160 165

Glu Tyr Pro Met Tyr Ser Gly Glu Lys Ala Tyr Ile Gln Gly Leu
170 175 180

Lys Glu Lys Phe Pro Gln Glu Glu Ala Ile Ile Asp Lys Tyr Ile
185 190 195

Lys Leu Val Lys Val Val Ser Ser Gly Ala Pro His Ala Ile Leu
200 205 210

Leu Lys Phe Leu Pro Leu Pro Val Val Gln Leu Leu Asp Arg Cys
215 220 225

Gly Leu Leu Thr Arg Phe Ser Pro Phe Leu Gln Ala Ser Thr Gln
230 235 240

Ser Leu Ala Glu Val Leu Gln Gln Leu Gly Ala Ser Ser Glu Leu
245 250 255

Gln Ala Val Leu Ser Tyr Ile Phe Pro Thr Tyr Gly Val Thr Pro
260 265 270

Asn His Ser Ala Phe Ser Met His Ala Leu Leu Val Asn His Tyr
275 280 285

Met Lys Gly Gly Phe Tyr Pro Arg Gly Gly Ser Ser Glu Ile Ala
290 295 300

Phe His Thr Ile Pro Val Ile Gln Arg Ala Gly Gly Ala Val Leu
305 310 315

Thr Lys Ala Thr Val Gln Ser Val Leu Leu Asp Ser Ala Gly Lys
320 325 330

Ala Cys Gly Val Ser Val Lys Lys Gly His Glu Leu Val Asn Ile
335 340 345

Tyr Cys Pro Ile Val Val Ser Asn Ala Gly Leu Phe Asn Thr Tyr
350 355 360

Glu His Leu Leu Pro Gly Asn Ala Arg Cys Leu Pro Gly Val Lys
365 370 375

Gln Gln Leu Gly Thr Val Arg Pro Gly Leu Gly Met Thr Ser Val
380 385 390

Phe Ile Cys Leu Arg Gly Thr Lys Glu Asp Leu His Leu Pro Ser
395 400 405

Thr Asn Tyr Tyr Val Tyr Tyr Asp Thr Asp Met Asp Gln Ala Met
410 415 420

Glu Arg Tyr Val Ser Met Pro Arg Glu Glu Ala Ala Glu His Ile
425 430 435

Pro Leu Leu Phe Phe Ala Phe Pro Ser Ala Lys Asp Pro Thr Trp
440 445 450

Glu Asp Arg Phe Pro Gly Arg Ser Thr Met Ile Met Leu Ile Pro
455 460 465

Thr Ala Tyr Glu Trp Phe Glu Glu Trp Gln Ala Glu Leu Lys Gly
470 475 480

Lys Arg Gly Ser Asp Tyr Glu Thr Phe Lys Asn Ser Phe Val Glu
485 490 495

Ala Ser Met Ser Val Val Leu Lys Leu Phe Pro Gln Leu Glu Gly
500 505 510

Lys Val Glu Ser Val Thr Ala Gly Ser Pro Leu Thr Asn Gln Phe
515 520 525

Tyr Leu Ala Ala Pro Arg Gly Ala Cys Tyr Gly Ala Asp His Asp
530 535 540

Leu Gly Arg Leu His Pro Cys Val Met Ala Ser Leu Arg Ala Gln
545 550 555

Ser Pro Ile Pro Asn Leu Tyr Leu Thr Gly Gln Asp Ile Phe Thr
560 565 570

Cys Gly Leu Val Gly Ala Leu Gln Gly Ala Leu Leu Cys Ser Ser
575 580 585

Ala Ile Leu Lys Arg Asn Leu Tyr Ser Asp Leu Lys Asn Leu Asp
590 595 600

Ser Arg Ile Arg Ala Gln Lys Lys Lys Asn
605 610

<210> 114
<211> 1701
<212> DNA
<213> Homo sapiens

<400> 114
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gatagggctg acgctgctgc tgtgtgcggt gctgctgagc ttggcctcgg 150

cgtcctcgga tgaagaaggc agccaggatg aatccttaga ttccaagact 200

actttgacat cagatgagtc agtaaaggac catactactg caggcagagt 250

agttgctggt caaatatttc ttgattcaga agaatctgaa ttagaatcct 300

ctattcaaga agaggaagac agcctcaaga gccaagaggg ggaaagtgtc 350

acagaagata tcagctttct agagtctcca aatccagaaa acaaggacta 400

tgaagagcca aagaaagtac ggaaaccagc tttgaccgcc attgaaggca 450

cagcacatgg ggagccctgc cacttccctt ttcttttcct agataaggag 500

tatgatgaat gtacatcaga tgggagggaa gatggcagac tgtggtgtgc 550

tacaacctat gactacaaag cagatgaaaa gtggggcttt tgtgaaactg 600

aagaagaggc tgctaagaga cggcagatgc aggaagcaga aatgatgtat 650

caaactggaa tgaaaatcct taatggaagc aataagaaaa gccaaaaaag 700

agaagcatat cggtatctcc aaaaggcagc aagcatgaac cataccaaag 750

ccctggagag agtgtcatat gctcttttat ttggtgatta cttgccacag 800

aatatccagg cagcgagaga gatgtttgag aagctgactg aggaaggctc 850

tcccaaggga cagactgctc ttggctttct gtatgcctct ggacttggtg 900

ttaattcaag tcaggcaaag gctcttgtat attatacatt tggagctctt 950

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gttgaacttc cttcaaattc ttgttaatgg atataacaca tggaatctac 1150

atgtaaatga aagttggtgg agtccacaat ttttctttaa aatgattagt 1200

ttggctgatt gcccctaaaa agagagatct gataaatggc tctttttaaa 1250

ttttctctga gttggaattg tcagaatcat tttttacatt agattatcat 1300

aattttaaaa atttttcttt agtttttcaa aattttgtaa atggtggcta 1350

tagaaaaaca acatgaaata ttatacaata ttttgcaaca atgccctaag 1400

aattgttaaa attcatggag ttatttgtgc agaatgactc cagagagctc 1450

tactttctgt tttttacttt tcatgattgg ctgtcttccc atttattctg 1500

gtcatttatt gctagtgaca ctgtgcctgc ttccagtagt ctcattttcc 1550

ctattttgct aatttgttac tttttctttg ctaatttgga agattaactc 1600

atttttaata aaattatgtc taagattaaa aaaaaaaaaa aaaaaaaaaa 1650

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700

a 1701

<210> 115
<211> 301
<212> PRT
<213> Homo sapiens

<400> 115

Met	Arg	Val	Arg	Ile	Gly	Leu	Thr	Leu	Leu	Leu	Cys	Ala	Val	Leu	
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Leu	Ser	Leu	Ala	Ser	Ala	Ser	Ser	Asp	Glu	Glu	Gly	Ser	Gln	Asp	
			20					25						30	

Glu Ser Leu Asp Ser Lys Thr Thr Leu Thr Ser Asp Glu Ser Val
35 40 45

Lys Asp His Thr Thr Ala Gly Arg Val Val Ala Gly Gln Ile Phe
50 55 60

Leu Asp Ser Glu Glu Ser Glu Leu Glu Ser Ser Ile Gln Glu Glu
65 70 75

Glu Asp Ser Leu Lys Ser Gln Glu Gly Glu Ser Val Thr Glu Asp
80 85 90

Ile Ser Phe Leu Glu Ser Pro Asn Pro Glu Asn Lys Asp Tyr Glu
95 100 105

Glu Pro Lys Lys Val Arg Lys Pro Ala Leu Thr Ala Ile Glu Gly
110 115 120

Thr Ala His Gly Glu Pro Cys His Phe Pro Phe Leu Phe Leu Asp
125 130 135

Lys Glu Tyr Asp Glu Cys Thr Ser Asp Gly Arg Glu Asp Gly Arg
140 145 150

Leu Trp Cys Ala Thr Thr Tyr Asp Tyr Lys Ala Asp Glu Lys Trp
155 160 165

Gly Phe Cys Glu Thr Glu Glu Glu Ala Ala Lys Arg Arg Gln Met
170 175 180

Gln Glu Ala Glu Met Met Tyr Gln Thr Gly Met Lys Ile Leu Asn
185 190 195

Gly Ser Asn Lys Lys Ser Gln Lys Arg Glu Ala Tyr Arg Tyr Leu
200 205 210

Gln Lys Ala Ala Ser Met Asn His Thr Lys Ala Leu Glu Arg Val
215 220 225

Ser Tyr Ala Leu Leu Phe Gly Asp Tyr Leu Pro Gln Asn Ile Gln
230 235 240

Ala Ala Arg Glu Met Phe Glu Lys Leu Thr Glu Glu Gly Ser Pro
245 250 255

Lys Gly Gln Thr Ala Leu Gly Phe Leu Tyr Ala Ser Gly Leu Gly
260 265 270

Val Asn Ser Ser Gln Ala Lys Ala Leu Val Tyr Tyr Thr Phe Gly
275 280 285

Ala Leu Gly Gly Asn Leu Ile Ala His Met Val Leu Val Ser Arg
290 295 300

Leu

<210> 116
<211> 584
<212> DNA
<213> Homo sapiens

<400> 116

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agctggatgc actgctggtc ttcccaggcc aagtggctca actctcctgc 200

acgctcagcc cccagcacgt caccatcagg gactacggtg tgtcctggta 250

ccagcagcgg gcaggcagtg cccctcgata tctcctctac taccgctcgg 300

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aggggtgggg tgtgagatgg gtgcctcccc tctgcctccc atttctgccc 500

ctgaccttgg gtccctttta aactttctct gagccttgct tcccctctgt 550

aaaatgggtt aataatattc aacatgtcaa caac 584

<210> 117
<211> 123
<212> PRT
<213> Homo sapiens

<400> 117

Met	Ala	Cys	Arg	Cys	Leu	Ser	Phe	Leu	Leu	Met	Gly	Thr	Phe	Leu	
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Ser	Val	Ser	Gln	Thr	Val	Leu	Ala	Gln	Leu	Asp	Ala	Leu	Leu	Val	
				20					25						30
Phe	Pro	Gly	Gln	Val	Ala	Gln	Leu	Ser	Cys	Thr	Leu	Ser	Pro	Gln	
				35					40						45
His	Val	Thr	Ile	Arg	Asp	Tyr	Gly	Val	Ser	Trp	Tyr	Gln	Gln	Arg	
				50					55						60
Ala	Gly	Ser	Ala	Pro	Arg	Tyr	Leu	Leu	Tyr	Tyr	Arg	Ser	Glu	Glu	
				65					70						75
Asp	His	His	Arg	Pro	Ala	Asp	Ile	Pro	Asp	Arg	Phe	Ser	Ala	Ala	
				80					85						90
Lys	Asp	Glu	Ala	His	Asn	Ala	Cys	Val	Leu	Thr	Ile	Ser	Pro	Val	
				95					100						105
Gln	Pro	Glu	Asp	Asp	Ala	Asp	Tyr	Tyr	Cys	Ser	Val	Gly	Tyr	Gly	
				110					115						120

Phe Ser Pro

<210> 118
<211> 3402
<212> DNA
<213> Homo sapiens

<400> 118

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tcctacctca ataagctgct catcacccgt gcccgccagg acgatgcggg 1150

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aatgcacgca cacgcacaga gacatgccag aacatacaag gacatgctgc 2000

ctgaacatac acacgcacac ccatgcgcag atgtgctgcc tggacacaca 2050

cacacacacg gatatgctgt ctggacgcac acacgtgcag atatggtatc 2100

cggacacaca cgtgcacaga tatgctgcct ggacacacag ataatgctgc 2150

cttgacacac acatgcacgg atattgcctg gacacacaca cacacacacg 2200

cgtgcacaga tatgctgtct ggacacgcac acacatgcag atatgctgcc 2250

tggacacaca cttccagaca cacgtgcaca ggcgcagata tgctgcctgg 2300

acacacgcag atatgctgtc tagtcacaca cacacgcaga catgctgtcc 2350

ggacacacac acgcatgcac agatatgctg tccggacaca cacacgcacg 2400

cagatatgct gcctggacac acacacagat aatgctgcct caacactcac 2450

acacgtgcag atattgcctg gacacacaca tgtgcacaga tatgctgtct 2500

ggacatgcac acacgtgcag atatgctgtc cggatacaca cgcacgcaca 2550

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gaaggaagac tgggttgcag ggactgtggt ctctcctggg gcccgggacc 3250

cgcctggtct ttcagccatg ctgatgacca caccccgtcc aggccagaca 3300

ccacccccca ccccactgtc gtggtggccc cagatctctg taattttatg 3350

tagagtttga gctgaagccc cgtatattta atttattttg ttaaacacaa 3400

aa 3402

<210> 119
<211> 504
<212> PRT
<213> Homo sapiens

<400> 119

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	
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Leu	Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	
				20				25						30	
Met	Ala	Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	
				35				40						45	
Thr	Val	Arg	Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	
				50				55						60	
Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	
				65				70						75	
Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	
				80				85						90	
Arg	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	
				95				100						105	
Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	
				110				115						120	
Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly	Gly	
				125				130						135	
Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg	Phe	Thr	
				140				145						150	
Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	
				155				160						165	
Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	
				170				175						180	
Asp	Ile	Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	
				185				190						195	
Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	
				200				205						210	
Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	
				215				220						225	
Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	
				230				235						240	

Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn
245 250 255

Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val
260 265 270

Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu
275 280 285

Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly
290 295 300

Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro
305 310 315

Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln
320 325 330

Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly
335 340 345

Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro Asp Pro Lys
350 355 360

Pro Pro Gly Pro Pro Val Ala Ser Ser Ser Ser Ala Thr Ser Leu
365 370 375

Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile
380 385 390

Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro
395 400 405

Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly His Arg Pro Pro
410 415 420

Gly Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu
425 430 435

Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu Glu His
440 445 450

Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro Val
455 460 465

Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr
470 475 480

His Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys
485 490 495

Val His Gln His Ile His Tyr Gln Cys
500

<210> 120
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 120

cgagatgacg ccgagccccc 20

<210> 121
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<400> 121
cggttcgaca cgcggcaggt g 21

<210> 122
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<400> 122
tgctgctcct gctgccgccg ctgctgctgg gggccttccc gccgg 45

<210> 123
<211> 4420
<212> DNA
<213> Homo sapiens

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gcctgggtgt tctccttcct ggtcctggaa gtcacatctg tgttggggag 200

acagacgatg ctcacccagt cagtaagaag agtccagcct gggaagaaga 250

accccagcat ctttgccaag cctgccgaca ccctggagag ccctggtgag 300

tggacaacat ggttcaacat cgactaccca ggcgggaagg gcgactatga 350

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gcagagactc catacatggt gatgaaccct gagacaaaag cacggagagc 1100

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<210> 124
<211> 1184
<212> PRT
<213> Homo sapiens

<400> 124

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				20				25						30	
Arg	Arg	Val	Gln	Pro	Gly	Lys	Lys	Asn	Pro	Ser	Ile	Phe	Ala	Lys	
				35				40						45	
Pro	Ala	Asp	Thr	Leu	Glu	Ser	Pro	Gly	Glu	Trp	Thr	Thr	Trp	Phe	
				50				55						60	
Asn	Ile	Asp	Tyr	Pro	Gly	Gly	Lys	Gly	Asp	Tyr	Glu	Arg	Leu	Asp	
				65				70						75	
Ala	Ile	Arg	Phe	Tyr	Tyr	Gly	Asp	Arg	Val	Cys	Ala	Arg	Pro	Leu	
				80				85						90	
Arg	Leu	Glu	Ala	Arg	Thr	Thr	Asp	Trp	Thr	Pro	Ala	Gly	Ser	Thr	
				95				100						105	
Gly	Gln	Val	Val	His	Gly	Ser	Pro	Arg	Glu	Gly	Phe	Trp	Cys	Leu	
				110				115						120	
Asn	Arg	Glu	Gln	Arg	Pro	Gly	Gln	Asn	Cys	Ser	Asn	Tyr	Thr	Val	
				125				130						135	
Arg	Phe	Leu	Cys	Pro	Pro	Gly	Ser	Leu	Arg	Arg	Asp	Thr	Glu	Arg	
				140				145						150	
Ile	Trp	Ser	Pro	Trp	Ser	Pro	Trp	Ser	Lys	Cys	Ser	Ala	Ala	Cys	
				155				160						165	
Gly	Gln	Thr	Gly	Val	Gln	Thr	Arg	Thr	Arg	Ile	Cys	Leu	Ala	Glu	
				170				175						180	
Met	Val	Ser	Leu	Cys	Ser	Glu	Ala	Ser	Glu	Glu	Gly	Gln	His	Cys	
				185				190						195	
Met	Gly	Gln	Asp	Cys	Thr	Ala	Cys	Asp	Leu	Thr	Cys	Pro	Met	Gly	
				200				205						210	

Gln Val Asn Ala Asp Cys Asp Ala Cys Met Cys Gln Asp Phe Met
215 220 225

Leu His Gly Ala Val Ser Leu Pro Gly Gly Ala Pro Ala Ser Gly
230 235 240

Ala Ala Ile Tyr Leu Leu Thr Lys Thr Pro Lys Leu Leu Thr Gln
245 250 255

Thr Asp Ser Asp Gly Arg Phe Arg Ile Pro Gly Leu Cys Pro Asp
260 265 270

Gly Lys Ser Ile Leu Lys Ile Thr Lys Val Lys Phe Ala Pro Ile
275 280 285

Val Leu Thr Met Pro Lys Thr Ser Leu Lys Ala Ala Thr Ile Lys
290 295 300

Ala Glu Phe Val Arg Ala Glu Thr Pro Tyr Met Val Met Asn Pro
305 310 315

Glu Thr Lys Ala Arg Arg Ala Gly Gln Ser Val Ser Leu Cys Cys
320 325 330

Lys Ala Thr Gly Lys Pro Arg Pro Asp Lys Tyr Phe Trp Tyr His
335 340 345

Asn Asp Thr Leu Leu Asp Pro Ser Leu Tyr Lys His Glu Ser Lys
350 355 360

Leu Val Leu Arg Lys Leu Gln Gln His Gln Ala Gly Glu Tyr Phe
365 370 375

Cys Lys Ala Gln Ser Asp Ala Gly Ala Val Lys Ser Lys Val Ala
380 385 390

Gln Leu Ile Val Thr Ala Ser Asp Glu Thr Pro Cys Asn Pro Val
395 400 405

Pro Glu Ser Tyr Leu Ile Arg Leu Pro His Asp Cys Phe Gln Asn
410 415 420

Ala Thr Asn Ser Phe Tyr Tyr Asp Val Gly Arg Cys Pro Val Lys
425 430 435

Thr Cys Ala Gly Gln Gln Asp Asn Gly Ile Arg Cys Arg Asp Ala
440 445 450

Val Gln Asn Cys Cys Gly Ile Ser Lys Thr Glu Glu Arg Glu Ile
455 460 465

Gln Cys Ser Gly Tyr Thr Leu Pro Thr Lys Val Ala Lys Glu Cys
470 475 480

Ser Cys Gln Arg Cys Thr Glu Thr Arg Ser Ile Val Arg Gly Arg
485 490 495

Val Ser Ala Ala Asp Asn Gly Glu Pro Met Arg Phe Gly His Val
500 505 510

Tyr Met Gly Asn Ser Arg Val Ser Met Thr Gly Tyr Lys Gly Thr
515 520 525

Phe Thr Leu His Val Pro Gln Asp Thr Glu Arg Leu Val Leu Thr
530 535 540

Phe Val Asp Arg Leu Gln Lys Phe Val Asn Thr Thr Lys Val Leu
545 550 555

Pro Phe Asn Lys Lys Gly Ser Ala Val Phe His Glu Ile Lys Met
560 565 570

Leu Arg Arg Lys Glu Pro Ile Thr Leu Glu Ala Met Glu Thr Asn
575 580 585

Ile Ile Pro Leu Gly Glu Val Val Gly Glu Asp Pro Met Ala Glu
590 595 600

Leu Glu Ile Pro Ser Arg Ser Phe Tyr Arg Gln Asn Gly Glu Pro
605 610 615

Tyr Ile Gly Lys Val Lys Ala Ser Val Thr Phe Leu Asp Pro Arg
620 625 630

Asn Ile Ser Thr Ala Thr Ala Ala Gln Thr Asp Leu Asn Phe Ile
635 640 645

Asn Asp Glu Gly Asp Thr Phe Pro Leu Arg Thr Tyr Gly Met Phe
650 655 660

Ser Val Asp Phe Arg Asp Glu Val Thr Ser Glu Pro Leu Asn Ala
665 670 675

Gly Lys Val Lys Val His Leu Asp Ser Thr Gln Val Lys Met Pro
680 685 690

Glu His Ile Ser Thr Val Lys Leu Trp Ser Leu Asn Pro Asp Thr
695 700 705

Gly Leu Trp Glu Glu Glu Gly Asp Phe Lys Phe Glu Asn Gln Arg
710 715 720

Arg Asn Lys Arg Glu Asp Arg Thr Phe Leu Val Gly Asn Leu Glu
725 730 735

Ile Arg Glu Arg Arg Leu Phe Asn Leu Asp Val Pro Glu Ser Arg
740 745 750

Arg Cys Phe Val Lys Val Arg Ala Tyr Arg Ser Glu Arg Phe Leu
755 760 765

Pro Ser Glu Gln Ile Gln Gly Val Val Ile Ser Val Ile Asn Leu
770 775 780

Glu Pro Arg Thr Gly Phe Leu Ser Asn Pro Arg Ala Trp Gly Arg
785 790 795

Phe Asp Ser Val Ile Thr Gly Pro Asn Gly Ala Cys Val Pro Ala
800 805 810

Phe Cys Asp Asp Gln Ser Pro Asp Ala Tyr Ser Ala Tyr Val Leu
815 820 825

Ala Ser Leu Ala Gly Glu Glu Leu Gln Ala Val Glu Ser Ser Pro
830 835 840

Lys Phe Asn Pro Asn Ala Ile Gly Val Pro Gln Pro Tyr Leu Asn
845 850 855

Lys Leu Asn Tyr Arg Arg Thr Asp His Glu Asp Pro Arg Val Lys
860 865 870

Lys Thr Ala Phe Gln Ile Ser Met Ala Lys Pro Arg Pro Asn Ser
875 880 885

Ala Glu Glu Ser Asn Gly Pro Ile Tyr Ala Phe Glu Asn Leu Arg
890 895 900

Ala Cys Glu Glu Ala Pro Pro Ser Ala Ala His Phe Arg Phe Tyr
905 910 915

Gln Ile Glu Gly Asp Arg Tyr Asp Tyr Asn Thr Val Pro Phe Asn
920 925 930

Glu Asp Asp Pro Met Ser Trp Thr Glu Asp Tyr Leu Ala Trp Trp
935 940 945

Pro Lys Pro Met Glu Phe Arg Ala Cys Tyr Ile Lys Val Lys Ile
950 955 960

Val Gly Pro Leu Glu Val Asn Val Arg Ser Arg Asn Met Gly Gly
965 970 975

Thr His Arg Arg Thr Val Gly Lys Leu Tyr Gly Ile Arg Asp Val
980 985 990

Arg Ser Thr Arg Asp Arg Asp Gln Pro Asn Val Ser Ala Ala Cys
995 1000 1005

Leu Glu Phe Lys Cys Ser Gly Met Leu Tyr Asp Gln Asp Arg Val
1010 1015 1020

Asp Arg Thr Leu Val Lys Val Ile Pro Gln Gly Ser Cys Arg Arg
1025 1030 1035

Ala Ser Val Asn Pro Met Leu His Glu Tyr Leu Val Asn His Leu
1040 1045 1050

Pro Leu Ala Val Asn Asn Asp Thr Ser Glu Tyr Thr Met Leu Ala
1055 1060 1065

Pro Leu Asp Pro Leu Gly His Asn Tyr Gly Ile Tyr Thr Val Thr
1070 1075 1080

Asp Gln Asp Pro Arg Thr Ala Lys Glu Ile Ala Leu Gly Arg Cys
1085 1090 1095

Phe Asp Gly Thr Ser Asp Gly Ser Ser Arg Ile Met Lys Ser Asn
1100 1105 1110

Val Gly Val Ala Leu Thr Phe Asn Cys Val Glu Arg Gln Val Gly
1115 1120 1125

Arg Gln Ser Ala Phe Gln Tyr Leu Gln Ser Thr Pro Ala Gln Ser
1130 1135 1140

Pro Ala Ala Gly Thr Val Gln Gly Arg Val Pro Ser Arg Arg Gln
1145 1150 1155

Gln Arg Ala Ser Arg Gly Gly Gln Arg Gln Gly Gly Val Val Ala
1160 1165 1170

Ser Leu Arg Phe Pro Arg Val Ala Gln Gln Pro Leu Ile Asn
1175 1180

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<210> 126
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<400> 126
ccattgtgca ggtcaggtca cag 23

<210> 127
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ctggagcaag tgctcagctg cctgtggtca gactggggtc 40

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tctgtgcaat gggcaatccc tacatgtgca ataatgagtg tgatgcgagt 550

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ctctccaggt taacatcact ctgtcttgga gcaaaaccat tgagctaaca 700

gacaacatag ttattacctt tgaatctggg cgtccagacc aaatgatcct 750

ggagaagtct ctcgattatg gacgaacatg gcagccctat cagtattatg 800

ccacagactg cttagatgct tttcacatgg atcctaaatc cgtgaaggat 850

ttatcacagc atacggtctt agaaatcatt tgcacagaag agtactcaac 900

agggtataca acaaatagca aaataatcca ctttgaaatc aaagacaggt 950

tcgcgctttt tgctggacct cgcctacgca atatggcttc cctctacgga 1000

cagctggata caaccaagaa actcagagat ttctttacag tcacagacct 1050

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gcaagaagaa ttatcagggc cgaccttgga gtccaggctc ctatctcccc 1300

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tacgaatgtc tgcgacaacg agctcctgca ctgccagaac ggagggacgt 1400

gccacaacaa cgtgcgctgc ctgtgcccgg ccgcatacac gggcatcctc 1450

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ccggacgggc ctgtgccgtg gggaagcaga cacaacccaa acatttgcta 1650

ctaacatagg aaacacacac atacagacac ccccactcag acagtgtaca 1700

aactaagaag gcctaactga actaagccat atttatcacc cgtggacagc 1750

acatccgagt caagactgtt aatttctgac tccagaggag ttggcagctg 1800

ttgatattat cactgcaaat cacattgcca gctgcagagc atattgtgga 1850

ttggaaaggc tgcgacagcc ccccaaacag gaaagacaaa aaacaaacaa 1900

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gactccgccc agtgtgtgga ccaaccaaat agcattcttt gctgtcaggt 2000

gcattgtggg cataaggaaa tctgttacaa gctgccatat tggcctgctt 2050

ccgtccctga atcccttcca acctgtgctt tagtgaacgt tgctctgtaa 2100

ccctcgttgg ttgaaagatt tctttgtctg atgttagtga tgcacatgtg 2150

taacagcccc ctctaaaagc gcaagccagt catacccctg tatatcttag 2200

cagcactgag tccagtgcga gcacacaccc actatacaag agtggctata 2250

ggaaaaaaga aagtgtatct atccttttgt attcaaatga agttattttt 2300

cttgaactac tgtaatatgt agatttttg tattattgcc aatttgtgtt 2350

accagacaat ctgttaatgt atctaattcg aatcagcaaa gactgacatt 2400

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tgtaagggca acgaacgtgc tggcatcaaa gaatatcagt ttacatatat 2500

aacaagtgta ataagattcc accaaaggac attctaaatg ttttcttgtt 2550

gctttaacac tggaagattt aaagaataaa aactcctgca taaacgattt 2600

caggaatttg tattgcaatt tcttaagatg aaaggaacag ccaccaagca 2650

gtttcacact cactttactg atttctgtgt ggactgagta cattcagctg 2700

acgaatttag ttcccaggaa gatggattga tgttcactag cttggacaac 2750

ttctgcaaaa tatgagacta tttccacttg ggaaaaatta caacagcaaa 2800

aaaaaaaaaa aaaaaaaaa 2819

<210> 129
<211> 438
<212> PRT
<213> Homo sapiens

<400> 129

Met	Tyr	Leu	Ser	Arg	Ser	Leu	Ser	Ile	His	Ala	Leu	Trp	Val	Thr	
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Val	Ser	Ser	Val	Met	Gln	Pro	Tyr	Pro	Leu	Val	Trp	Gly	His	Tyr	
				20				25						30	
Asp	Leu	Cys	Lys	Thr	Gln	Ile	Tyr	Thr	Glu	Glu	Gly	Lys	Val	Trp	
				35				40						45	
Asp	Tyr	Met	Ala	Cys	Gln	Pro	Glu	Ser	Thr	Asp	Met	Thr	Lys	Tyr	
				50				55						60	
Leu	Lys	Val	Lys	Leu	Asp	Pro	Pro	Asp	Ile	Thr	Cys	Gly	Asp	Pro	
				65				70						75	
Pro	Glu	Thr	Phe	Cys	Ala	Met	Gly	Asn	Pro	Tyr	Met	Cys	Asn	Asn	
				80				85						90	
Glu	Cys	Asp	Ala	Ser	Thr	Pro	Glu	Leu	Ala	His	Pro	Pro	Glu	Leu	
				95				100						105	
Met	Phe	Asp	Phe	Glu	Gly	Arg	His	Pro	Ser	Thr	Phe	Trp	Gln	Ser	
				110				115						120	

Ala Thr Trp Lys Glu Tyr Pro Lys Pro Leu Gln Val Asn Ile Thr

125 130 135

Leu Ser Trp Ser Lys Thr Ile Glu Leu Thr Asp Asn Ile Val Ile
140 145 150

Thr Phe Glu Ser Gly Arg Pro Asp Gln Met Ile Leu Glu Lys Ser
155 160 165

Leu Asp Tyr Gly Arg Thr Trp Gln Pro Tyr Gln Tyr Tyr Ala Thr
170 175 180

Asp Cys Leu Asp Ala Phe His Met Asp Pro Lys Ser Val Lys Asp
185 190 195

Leu Ser Gln His Thr Val Leu Glu Ile Ile Cys Thr Glu Glu Tyr
200 205 210

Ser Thr Gly Tyr Thr Thr Asn Ser Lys Ile Ile His Phe Glu Ile
215 220 225

Lys Asp Arg Phe Ala Leu Phe Ala Gly Pro Arg Leu Arg Asn Met
230 235 240

Ala Ser Leu Tyr Gly Gln Leu Asp Thr Thr Lys Lys Leu Arg Asp
245 250 255

Phe Phe Thr Val Thr Asp Leu Arg Ile Arg Leu Leu Arg Pro Ala
260 265 270

Val Gly Glu Ile Phe Val Asp Glu Leu His Leu Ala Arg Tyr Phe
275 280 285

Tyr Ala Ile Ser Asp Ile Lys Val Arg Gly Arg Cys Lys Cys Asn
290 295 300

Leu His Ala Thr Val Cys Val Tyr Asp Asn Ser Lys Leu Thr Cys
305 310 315

Glu Cys Glu His Asn Thr Thr Gly Pro Asp Cys Gly Lys Cys Lys
320 325 330

Lys Asn Tyr Gln Gly Arg Pro Trp Ser Pro Gly Ser Tyr Leu Pro
335 340 345

Ile Pro Lys Gly Thr Ala Asn Thr Cys Ile Pro Ser Ile Ser Ser
350 355 360

Ile Gly Thr Asn Val Cys Asp Asn Glu Leu Leu His Cys Gln Asn
365 370 375

Gly Gly Thr Cys His Asn Asn Val Arg Cys Leu Cys Pro Ala Ala
380 385 390

Tyr Thr Gly Ile Leu Cys Glu Lys Leu Arg Cys Glu Glu Ala Gly
395 400 405

Ser Cys Gly Ser Asp Ser Gly Gln Gly Ala Pro Pro His Gly Thr
410 415 420

Pro Ala Leu Leu Leu Leu Thr Thr Leu Leu Gly Thr Ala Ser Pro
425 430 435

Leu Val Phe

<210> 130
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 130
tcgattatgg acgaacatgg cagc 24

<210> 131
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 131
ttctgagatc cctcatcctc 20

<210> 132
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 132
aggttcaggg acagcaagtt tggg 24

<210> 133
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 133
tttgctggac ctcggctacg gaattggctt ccctctacgg acagctggat 50

<210> 134
<211> 1493
<212> DNA
<213> Homo sapiens

<400> 134
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ccgggcgagg tgtcctcatg acttctcttg tggaccatgt ccgtgatctt 150

ttttgcctgc gtggtacggg taagggatgg actgcccctc tcagcctcta 200

ctgattttta ccacacccaa gatttttttgg aatggaggag acggctcaag 250

agtttagcct tgcgactggc ccagtatcca ggtcgaggtt ctgcagaagg 300

ttgtgacttt agtatacatt tttcttcttt cggggacgtg gcctgcatgg 350

ctatctgctc ctgccagtgt ccagcagcca tggccttctg cttcctggag 400

accctgtggt gggaattcac agcttcctat gacactacct gcattggcct 450

agcctccagg ccatacgctt ttcttgagtt tgacagcatc attcagaaag 500

tgaagtggca ttttaactat gtaagttcct ctcagatgga gtgcagcttg 550

gaaaaaattc aggaggagct caagttgcag cctccagcgg ttctcactct 600

ggaggacaca gatgtggcaa atggggtgat gaatggtcac acaccgatgc 650

acttggagcc tgctcctaat ttccgaatgg aaccagtgac agccctgggt 700

atcctctccc tcattctcaa catcatgtgt gctgccctga atctcattcg 750

aggagttcac cttgcagaac attctttaca ggatccaagg agctggttct 800

gctggttgga ccaaacctcg tgagccagcc acccctgacc caaatgagga 850

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gggaaatctc atcagcaggg agcctgtgga aaagggcatg tcagtgaaat 950

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ctattcctct gacccatgct tagtacatat gacctttaac ccttacattt 1100

atatgattct ggggttgctt cagaagtgtt atttcatgaa tcattcatat 1150

gatttgatcc cccaggattc tattttgttt aatgggcttt tctactaaaa 1200

gcataaaata ctgaggctga tttagtcagg gcaaaaccat ttactttaca 1250

tattcgtttt caatacttgc tgttcatgtt acacaagctt cttacggttt 1300

tcttgtaaca ataaatattt tgagtaaata atgggtacat tttaacaaac 1350

tcagtagtac aacctaaact tgtataaaag tgtgtaaaaa tgtatagcca 1400

tttatatcct atgtataaat taaatgaggt ggcttcagaa atggcagaat 1450

aaatctaaag tgtttattaa aaaaaaaaaa aaaaaaaaaa aag 1493

<210> 135
<211> 228
<212> PRT
<213> Homo sapiens

<400> 135

Met	Ser	Val	Ile	Phe	Phe	Ala	Cys	Val	Val	Arg	Val	Arg	Asp	Gly	
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Leu	Pro	Leu	Ser	Ala	Ser	Thr	Asp	Phe	Tyr	His	Thr	Gln	Asp	Phe	
				20				25						30	
Leu	Glu	Trp	Arg	Arg	Arg	Leu	Lys	Ser	Leu	Ala	Leu	Arg	Leu	Ala	
				35				40						45	

Gln Tyr Pro Gly Arg Gly Ser Ala Glu Gly Cys Asp Phe Ser Ile
50 55 60

His Phe Ser Ser Phe Gly Asp Val Ala Cys Met Ala Ile Cys Ser
65 70 75

Cys Gln Cys Pro Ala Ala Met Ala Phe Cys Phe Leu Glu Thr Leu
80 85 90

Trp Trp Glu Phe Thr Ala Ser Tyr Asp Thr Thr Cys Ile Gly Leu
95 100 105

Ala Ser Arg Pro Tyr Ala Phe Leu Glu Phe Asp Ser Ile Ile Gln
110 115 120

Lys Val Lys Trp His Phe Asn Tyr Val Ser Ser Ser Gln Met Glu
125 130 135

Cys Ser Leu Glu Lys Ile Gln Glu Glu Leu Lys Leu Gln Pro Pro
140 145 150

Ala Val Leu Thr Leu Glu Asp Thr Asp Val Ala Asn Gly Val Met
155 160 165

Asn Gly His Thr Pro Met His Leu Glu Pro Ala Pro Asn Phe Arg
170 175 180

Met Glu Pro Val Thr Ala Leu Gly Ile Leu Ser Leu Ile Leu Asn
185 190 195

Ile Met Cys Ala Ala Leu Asn Leu Ile Arg Gly Val His Leu Ala
200 205 210

Glu His Ser Leu Gln Asp Pro Arg Ser Trp Phe Cys Trp Leu Asp
215 220 225

Gln Thr Ser

<210> 136
<211> 239
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 39, 61, 143, 209
<223> unknown base

<400> 136
tgcttcctgg agaccctgtg gtgggaattc acagcttcnt atgacactac 50

ctgcattggc ntagcctcca ggccatacgc ttttcttgag tttgacagca 100

tcattcagaa agtgaagtgg cattttaact atgtaagttc ctntcagatg 150

gagtgcagct tggaaaaaat tcaggaggag ctcaagttgc agcctccagc 200

ggttctcant atggaggaca cagatgtggc aaatggggt 239

<210> 137
<211> 2300
<212> DNA

<213> Homo sapiens

<400> 137
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acgtgagcgc gacccgacct taaagagtgg ggagcaaagg gaggacagag 100

ccctttaaaa cgaggcgggt ggtgcctgcc cctttaaggg cggggcgtcc 150

ggacgactgt atctgagccc cagactgccc cgagtttctg tcgcaggctg 200

cgaggaaagg cccctaggct gggtctgggt gcttggcggc ggcggcttcc 250

tccccgctcg tcctccccgg gcccagaggc acctcggctt cagtcatgct 300

gagcagagta tggaagcacc tgactacgaa gtgctatccg tgcgagaaca 350

gctattccac gagaggatcc gcgagtgtat tatatcaaca cttctgtttg 400

caacactgta catcctctgc cacatcttcc tgacccgctt caagaagcct 450

gctgagttca ccacagtgga tgatgaagat gccaccgtca acaagattgc 500

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aactactaca tccagtggct caacggctcc ctcatccatg gcctctggaa 650

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catatttctt cactgagtct gagggctttg ctggctccag aaagggtgtc 750

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ggtgctaggt atggtgtggg tggcatcagc cattgtggac aagaacaagg 850

ccaacagaga gtcactctat gacttttggg agtactatct cccctacctc 900

tactcatgca tctccttcct tggggttctg ctgctcctgg tgtgtactcc 950

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gcaatttcta cattgtgttc ctctacaacg cagcctttgc aggcctcacc 1650

acactctgtc tggtgaagac cttcactgca gctgtgcggg cagagctgat 1700

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gaggaggagg cttcagccat cagcaataaa gttgatccca gggaaaaaaa 2300

<210> 138
<211> 489
<212> PRT
<213> Homo sapiens

<400> 138

Met	Glu	Ala	Pro	Asp	Tyr	Glu	Val	Leu	Ser	Val	Arg	Glu	Gln	Leu	
1				5				10						15	
Phe	His	Glu	Arg	Ile	Arg	Glu	Cys	Ile	Ile	Ser	Thr	Leu	Leu	Phe	
				20				25						30	
Ala	Thr	Leu	Tyr	Ile	Leu	Cys	His	Ile	Phe	Leu	Thr	Arg	Phe	Lys	
				35				40						45	
Lys	Pro	Ala	Glu	Phe	Thr	Thr	Val	Asp	Asp	Glu	Asp	Ala	Thr	Val	
				50				55						60	
Asn	Lys	Ile	Ala	Leu	Glu	Leu	Cys	Thr	Phe	Thr	Leu	Ala	Ile	Ala	
				65				70						75	
Leu	Gly	Ala	Val	Leu	Leu	Leu	Pro	Phe	Ser	Ile	Ile	Ser	Asn	Glu	
				80				85						90	
Val	Leu	Leu	Ser	Leu	Pro	Arg	Asn	Tyr	Tyr	Ile	Gln	Trp	Leu	Asn	
				95				100						105	
Gly	Ser	Leu	Ile	His	Gly	Leu	Trp	Asn	Leu	Val	Phe	Leu	Phe	Pro	
				110				115						120	
Asn	Leu	Ser	Leu	Ile	Phe	Leu	Met	Pro	Phe	Ala	Tyr	Phe	Phe	Thr	

125 130 135

Glu Ser Glu Gly Phe Ala Gly Ser Arg Lys Gly Val Leu Gly Arg
140 145 150

Val Tyr Glu Thr Val Val Met Leu Met Leu Leu Thr Leu Leu Val
155 160 165

Leu Gly Met Val Trp Val Ala Ser Ala Ile Val Asp Lys Asn Lys
170 175 180

Ala Asn Arg Glu Ser Leu Tyr Asp Phe Trp Glu Tyr Tyr Leu Pro
185 190 195

Tyr Leu Tyr Ser Cys Ile Ser Phe Leu Gly Val Leu Leu Leu Leu
200 205 210

Val Cys Thr Pro Leu Gly Leu Ala Arg Met Phe Ser Val Thr Gly
215 220 225

Lys Leu Leu Val Lys Pro Arg Leu Leu Glu Asp Leu Glu Glu Gln
230 235 240

Leu Tyr Cys Ser Ala Phe Glu Glu Ala Ala Leu Thr Arg Arg Ile
245 250 255

Cys Asn Pro Thr Ser Cys Trp Leu Pro Leu Asp Met Glu Leu Leu
260 265 270

His Arg Gln Val Leu Ala Leu Gln Thr Gln Arg Val Leu Leu Glu
275 280 285

Lys Arg Arg Lys Ala Ser Ala Trp Gln Arg Asn Leu Gly Tyr Pro
290 295 300

Leu Ala Met Leu Cys Leu Leu Val Leu Thr Gly Leu Ser Val Leu
305 310 315

Ile Val Ala Ile His Ile Leu Glu Leu Leu Ile Asp Glu Ala Ala
320 325 330

Met Pro Arg Gly Met Gln Gly Thr Ser Leu Gly Gln Val Ser Phe
335 340 345

Ser Lys Leu Gly Ser Phe Gly Ala Val Ile Gln Val Val Leu Ile
350 355 360

Phe Tyr Leu Met Val Ser Ser Val Val Gly Phe Tyr Ser Ser Pro
365 370 375

Leu Phe Arg Ser Leu Arg Pro Arg Trp His Asp Thr Ala Met Thr
380 385 390

Gln Ile Ile Gly Asn Cys Val Cys Leu Leu Val Leu Ser Ser Ala
395 400 405

Leu Pro Val Phe Ser Arg Thr Leu Gly Leu Thr Arg Phe Asp Leu
410 415 420

Leu Gly Asp Phe Gly Arg Phe Asn Trp Leu Gly Asn Phe Tyr Ile
425 430 435

Val Phe Leu Tyr Asn Ala Ala Phe Ala Gly Leu Thr Thr Leu Cys

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440 445 450

Leu Val Lys Thr Phe Thr Ala Ala Val Arg Ala Glu Leu Ile Arg
455 460 465

Ala Phe Gly Leu Asp Arg Leu Pro Leu Pro Val Ser Gly Phe Pro
470 475 480

Gln Ala Ser Arg Lys Thr Gln His Gln
485

<210> 139
<211> 294
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 53, 57
<223> unknown base

<400> 139
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ggnttcntcc ccgctcgtcc tccccgggcc cagaggcacc tcggcttcag 100

tcatgctgag cagagtatgg aagcacctga ctacgaagtg ctatccgtgc 150

gagaacagct attccacgag aggatccgcg agtgtattat atcaacactt 200

ctgtttgcaa cactgtacat cctctgccac atcttcctga cccgcttcaa 250

gaagcctgct gagttcacca cagtggatga tgaagatgcc accg 294

<210> 140
<211> 526
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 197, 349
<223> unknown base

<400> 140
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aggcggtggt gcctgccctt taagggcggg gcgtccggac gactgtatct 100

gagccccaga ctgccccgag tttctgtcgc aggctgcgag gaaaggcccc 150

taggctgggt ctggtgcttg gcggcggcgg cttcctcccc gttgtcntcc 200

ccgggcccag aggcacctcg gcttcagtca tgctgagcag agtatggaag 250

cacctgacta cgaagtgcta tccgtgcgag aacagctatt ccacgagagg 300

atccgcgagt gtattatatc aacacttctg tttgcaacac tgtacatcnt 350

ctgccacatc ttcctgaccc gcttcaagaa gcctgctgag ttcaccacag 400

tggatgatga agatgccacc gtcaacaaga ttgcgctcga gctgtgcacc 450

tttaccctgg caattgccct gggtgctgtc ctgctcctgc ccttctccat 500

catcagcaat gaggtgctgc actccc 526

<210> 141
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 141
gactgtatct gagccccaga ctgc 24

<210> 142
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 142
tcagcaatga ggtgctgctc 20

<210> 143
<211> 24
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 143
tgaggaagat gagggacagg ttgg 24

<210> 144
<211> 50
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 144
tatggaagca cctgactacg aagtgctatc cgtgcgagaa cagctattcc 50

<210> 145
<211> 685
<212> DNA
<213> Homo sapiens

<400> 145
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caaacctgtt ttggaattga ggaaacttct cttttgatct cagcccttgg 100

tggtccaggt cttcatgctg ctgtgggtga tattactggt cctggctcct 150

gtcagtggac agtttgcaag gacacccagg cccattattt tcctccagcc 200

tccatggacc acagtcttcc aaggagagag agtgaccctc acttgcaagg 250

gatttcgctt ctactcacca cagaaaacaa aatggtacca tcggtacctt 300

gggaaagaaa tactaagaga aaccccagac aatatccttg aggttcagga 350

atctggagag tacagatgcc aggcccaggg ctcccctctc agtagccctg 400

tgcacttgga tttttcttca gagatgggat ttcctcatgc tgcccaggct 450

aatgttgaac tcctgggctc aagtgatctg ctcacctagg cctctcaaag 500

cgctgggatt acagcttcgc tgatcctgca agctccactt tctgtgtttg 550

aaggagactc tgtggttctg aggtgccggg caaaggcgga agtaacactg 600

aataatacta tttacaagaa tgataatgtc ctggcattcc ttaataaaag 650

aactgacttc caaaaaaaaa aaaaaaaaaa aaaaa 685

<210> 146
<211> 124
<212> PRT
<213> Homo sapiens

<400> 146

Met	Leu	Leu	Trp	Val	Ile	Leu	Leu	Val	Leu	Ala	Pro	Val	Ser	Gly	
1				5				10						15	
Gln	Phe	Ala	Arg	Thr	Pro	Arg	Pro	Ile	Ile	Phe	Leu	Gln	Pro	Pro	
			20					25						30	
Trp	Thr	Thr	Val	Phe	Gln	Gly	Glu	Arg	Val	Thr	Leu	Thr	Cys	Lys	
			35					40						45	
Gly	Phe	Arg	Phe	Tyr	Ser	Pro	Gln	Lys	Thr	Lys	Trp	Tyr	His	Arg	
			50					55						60	
Tyr	Leu	Gly	Lys	Glu	Ile	Leu	Arg	Glu	Thr	Pro	Asp	Asn	Ile	Leu	
			65					70						75	
Glu	Val	Gln	Glu	Ser	Gly	Glu	Tyr	Arg	Cys	Gln	Ala	Gln	Gly	Ser	
			80					85						90	
Pro	Leu	Ser	Ser	Pro	Val	His	Leu	Asp	Phe	Ser	Ser	Glu	Met	Gly	
			95					100						105	
Phe	Pro	His	Ala	Ala	Gln	Ala	Asn	Val	Glu	Leu	Leu	Gly	Ser	Ser	
			110					115						120	

Asp Leu Leu Thr

<210> 147
<211> 1621
<212> DNA
<213> Homo sapiens

<400> 147
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ccccccccggt gtgaggcggc ctcacagggc cgggtgggct ggcgagccga 100

cgcggcggcg gaggaggctg tgaggagtgt gtggaacagg acccgggaca 150

gaggaaccat ggctccgcag aacctgagca ccttttgcct gttgctgcta 200

tacctcatcg gggcggtgat tgccggacga gatttctata agatcttggg 250

ggtgcctcga agtgcctcta taaaggatat taaaaaggcc tataggaaac 300

tagccctgca gcttcatccc gaccggaacc ctgatgatcc acaagcccag 350

gagaaattcc aggatctggg tgctgcttat gaggttctgt cagatagtga 400

gaaacggaaa cagtacgata cttatggtga agaaggatta aaagatggtc 450

atcagagctc ccatggagac atttttcac acttctttgg ggattttggt 500

ttcatgtttg gaggaacccc tcgtcagcaa gacagaaata ttccaagagg 550

aagtgatatt attgtagatc tagaagtcac tttggaagaa gtatatgcag 600

gaaattttgt ggaagtagtt agaaacaaac ctgtggcaag gcaggctcct 650

ggcaaacgga agtgcaattg tcggcaagag atgcggacca cccagctggg 700

ccctgggcgc ttccaaatga cccaggaggt ggtctgcgac gaatgcccta 750

atgtcaaact agtgaatgaa gaacgaacgc tggaagtaga aatagagcct 800

ggggtgagag acggcatgga gtaccccttt attggagaag gtgagcctca 850

cgtggatggg gagcctggag atttacggtt ccgaatcaaa gttgtcaagc 900

acccaatatt tgaaaggaga ggagatgatt tgtacacaaa tgtgacaatc 950

tcattagttg agtcactggt tggctttgag atggatatta ctcacttgga 1000

tggtcacaag gtacatattt cccgggataa gatcaccagg ccaggagcga 1050

agctatggaa gaaaggggaa gggctcccca actttgacaa caacaatatc 1100

aagggctctt tgataatcac ttttgatgtg gattttccaa aagaacagtt 1150

aacagaggaa gcgagagaag gtatcaaaca gctactgaaa caagggtcag 1200

tgcagaaggt atacaatgga ctgcaaggat attgagagtg aataaaattg 1250

gactttgttt aaaataagtg aataagcgat atttattatc tgcaaggttt 1300

ttttgtgtgt gtttttgttt ttattttcaa tatgcaagtt aggcttaatt 1350

tttttatcta atgatcatca tgaaatgaat aagagggctt aagaatttgt 1400

ccatttgcat tcggaaaaga atgaccagca aaaggtttac taatacctct 1450

ccctttgggg atttaatgtc tggtgctgcc gcctgagttt caagaattaa 1500

agctgcaaga ggactccagg agcaaaagaa acacaatata gagggttgga 1550

gttgttagca atttcattca aaatgccaac tggagaagtc tgtttttaaa 1600

tacattttgt tgttattttt a 1621

<210> 148
<211> 358
<212> PRT

<213> Homo sapiens

<400> 148

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Met Ala Pro Gln Asn Leu Ser Thr Phe Cys Leu Leu Leu Leu Tyr
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Leu Ile Gly Ala Val Ile Ala Gly Arg Asp Phe Tyr Lys Ile Leu
            20                  25                  30

Gly Val Pro Arg Ser Ala Ser Ile Lys Asp Ile Lys Lys Ala Tyr
        35                  40                  45

Arg Lys Leu Ala Leu Gln Leu His Pro Asp Arg Asn Pro Asp Asp
    50                  55                  60

Pro Gln Ala Gln Glu Lys Phe Gln Asp Leu Gly Ala Ala Tyr Glu
65                  70                  75

Val Leu Ser Asp Ser Glu Lys Arg Lys Gln Tyr Asp Thr Tyr Gly
                80                  85                  90

Glu Glu Gly Leu Lys Asp Gly His Gln Ser Ser His Gly Asp Ile
            95                  100                 105

Phe Ser His Phe Phe Gly Asp Phe Gly Phe Met Phe Gly Gly Thr
        110                 115                 120

Pro Arg Gln Gln Asp Arg Asn Ile Pro Arg Gly Ser Asp Ile Ile
    125                 130                 135

Val Asp Leu Glu Val Thr Leu Glu Glu Val Tyr Ala Gly Asn Phe
140                 145                 150

Val Glu Val Val Arg Asn Lys Pro Val Ala Arg Gln Ala Pro Gly
155                 160                 165

Lys Arg Lys Cys Asn Cys Arg Gln Glu Met Arg Thr Thr Gln Leu
                170                 175                 180

Gly Pro Gly Arg Phe Gln Met Thr Gln Glu Val Val Cys Asp Glu
            185                 190                 195

Cys Pro Asn Val Lys Leu Val Asn Glu Glu Arg Thr Leu Glu Val
        200                 205                 210

Glu Ile Glu Pro Gly Val Arg Asp Gly Met Glu Tyr Pro Phe Ile
    215                 220                 225

Gly Glu Gly Glu Pro His Val Asp Gly Glu Pro Gly Asp Leu Arg
230                 235                 240

Phe Arg Ile Lys Val Val Lys His Pro Ile Phe Glu Arg Arg Gly
                245                 250                 255

Asp Asp Leu Tyr Thr Asn Val Thr Ile Ser Leu Val Glu Ser Leu
            260                 265                 270

Val Gly Phe Glu Met Asp Ile Thr His Leu Asp Gly His Lys Val
        275                 280                 285

His Ile Ser Arg Asp Lys Ile Thr Arg Pro Gly Ala Lys Leu Trp
    290                 295                 300
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Lys Lys Gly Glu Gly Leu Pro Asn Phe Asp Asn Asn Asn Ile Lys
305 310 315

Gly Ser Leu Ile Ile Thr Phe Asp Val Asp Phe Pro Lys Glu Gln
320 325 330

Leu Thr Glu Glu Ala Arg Glu Gly Ile Lys Gln Leu Leu Lys Gln
335 340 345

Gly Ser Val Gln Lys Val Tyr Asn Gly Leu Gln Gly Tyr
350 355

<210> 149
<211> 509
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 34, 52, 134, 142, 155, 158, 196, 217, 228, 272, 347, 410, 445, 482
<223> unknown base

<400> 149
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gntgcgaccg aagcggcggg cggaggaggt tttgaggatt tttggaacag 100

gacccggaca gaggaaccat ggttccgcag aacntgagca cnttttgcct 150

gttgntgnta tacttcatcg gggcggtgat tgccggacga gatttntata 200

agattttggg gtgcctngaa gtgccttnta taaaggatat taaaaaggcc 250

tataggaaac tagccctgca gntttatccc gaccggaacc ctgatgatcc 300

acaagcccag gagaaattcc aggatttggg tgctgcttat gaggttntgt 350

cagatagtga gaaacggaaa cagtacgata attatggtga agaaggatta 400

aaagatggtn atcagagctc ccatggagac atttttttcac acttntttgg 450

ggattttggt ttcatgtttg gaggaacccc tngtcagcaa gacagaaata 500

ttccaagag 509

<210> 150
<211> 1532
<212> DNA
<213> Homo sapiens

<400> 150
ggcacgaggc ggcggggcag tcgcgggatg cgcccgggag ccacagcctg 50

aggccctcag gtctctgcag gtgtcgtgga ggaacctagc acctgccatc 100

ctcttcccca atttgccact tccagcagct ttagcccatg aggaggatgt 150

gaccgggact gagtcaggag ccctctggaa gcatggagac tgtggtgatt 200

gttgccatag gtgtgctggc caccatcttt ctggcttcgt ttgcagcctt 250

ggtgctggtt tgcaggcagc gctactgccg gccgcgagac ctgctgcagc 300

gctatgattc taagcccatt gtggacctca ttggtgccat ggagacccag 350

tctgagccct ctgagttaga actggacgat gtcgttatca ccaaccccca 400

cattgaggcc attctggaga atgaagactg gatcgaagat gcctcgggtc 450

tcatgtccca ctgcattgcc atcttgaaga tttgtcacac tctgacagag 500

aagcttgttg ccatgacaat gggctctggg gccaagatga agacttcagc 550

cagtgtcagc gacatcattg tggtggccaa gcggatcagc cccagggtgg 600

atgatgttgt gaagtcgatg taccctccgt tggaccccaa actcctggac 650

gcacggacga ctgccctgct cctgtctgtc agtcacctgg tgctggtgac 700

aaggaatgcc tgccatctga cgggaggcct ggactggatt gaccagtctc 750

tgtcggctgc tgaggagcat ttggaagtcc ttcgagaagc agccctagct 800

tctgagccag ataaaggcct cccaggccct gaaggcttcc tgcaggagca 850

gtctgcaatt tagtgcctac aggccagcag ctagccatga aggcccctgc 900

cgccatccct ggatggctca gcttagcctt ctacttttc ctatagagtt 950

agttgttctc cacggctgga gagttcagct gtgtgtgcat agtaaagcag 1000

gagatccccg tcagtttatg cctcttttgc agttgcaaac tgtggctggt 1050

gagtggcagt ctaatactac agttagggga gatgccattc actctctgca 1100

agaggagtat tgaaaactgg tggactgtca gctttattta gctcacctag 1150

tgttttcaag aaaattgagc caccgtctaa gaaatcaaga ggtttcacat 1200

taaaattaga atttctggcc tctctcgatc ggtcagaatg tgtggcaatt 1250

ctgatctgca ttttcagaag aggacaatca attgaaacta agtaggggtt 1300

tcttcttttg gcaagacttg tactctctca cctggcctgt ttcatttatt 1350

tgtattatct gcctggtccc tgaggcgtct gggtctctcc tctcccttgc 1400

aggtttgggt ttgaagctga ggaactacaa agttgatgat ttctttttta 1450

tctttatgcc tgcaatttta cctagctacc actaggtgga tagtaaattt 1500

atacttatgt ttccctcaaa aaaaaaaaaa aa 1532

<210> 151
<211> 226
<212> PRT
<213> Homo sapiens

<400> 151

Met	Glu	Thr	Val	Val	Ile	Val	Ala	Ile	Gly	Val	Leu	Ala	Thr	Ile	
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Phe	Leu	Ala	Ser	Phe	Ala	Ala	Leu	Val	Leu	Val	Cys	Arg	Gln	Arg	
			20					25						30	
Tyr	Cys	Arg	Pro	Arg	Asp	Leu	Leu	Gln	Arg	Tyr	Asp	Ser	Lys	Pro	

35 40 45

Ile Val Asp Leu Ile Gly Ala Met Glu Thr Gln Ser Glu Pro Ser
50 55 60

Glu Leu Glu Leu Asp Asp Val Val Ile Thr Asn Pro His Ile Glu
65 70 75

Ala Ile Leu Glu Asn Glu Asp Trp Ile Glu Asp Ala Ser Gly Leu
80 85 90

Met Ser His Cys Ile Ala Ile Leu Lys Ile Cys His Thr Leu Thr
95 100 105

Glu Lys Leu Val Ala Met Thr Met Gly Ser Gly Ala Lys Met Lys
110 115 120

Thr Ser Ala Ser Val Ser Asp Ile Ile Val Val Ala Lys Arg Ile
125 130 135

Ser Pro Arg Val Asp Asp Val Val Lys Ser Met Tyr Pro Pro Leu
140 145 150

Asp Pro Lys Leu Leu Asp Ala Arg Thr Thr Ala Leu Leu Leu Ser
155 160 165

Val Ser His Leu Val Leu Val Thr Arg Asn Ala Cys His Leu Thr
170 175 180

Gly Gly Leu Asp Trp Ile Asp Gln Ser Leu Ser Ala Ala Glu Glu
185 190 195

His Leu Glu Val Leu Arg Glu Ala Ala Leu Ala Ser Glu Pro Asp
200 205 210

Lys Gly Leu Pro Gly Pro Glu Gly Phe Leu Gln Glu Gln Ser Ala
215 220 225

Ile

<210> 152
<211> 1027
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1017, 1020
<223> unknown base

<400> 152
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tcgccgctgt ccccaccact gcagccatga tctccttaac ggacacgcag 100

aaaattggaa tgggattaac aggatttgga gtgtttttcc tgttctttgg 150

aatgattctc ttttttgaca aagcactact ggctattgga aatgttttat 200

ttgtagccgg cttggctttt gtaattggtt tagaaagaac attcagattc 250

ttcttccaaa aacataaaat gaaagctaca ggtttttttc tgggtggtgt 300

atttgtagtc cttattggtt ggcctttgat aggcatgatc ttcgaaattt 350

atggattttt tctcttgttc aggggcttct ttcctgtcgt tgttggcttt 400

attagaagag tgccagtcct tggatccctc ctaaatttac ctggaattag 450

atcatttgta gataaagttg gagaaagcaa caatatggta taacaacaag 500

tgaatttgaa gactcattta aaatattgtg ttatttataa agtcatttga 550

agaatattca gcacaaaatt aaattacatg aaatagcttg taatgttctt 600

tacaggagtt taaaacgtat agcctacaaa gtaccagcag caaattagca 650

aagaagcagt gaaaacaggc ttctactcaa gtgaactaag aagaagtcag 700

caagcaaact gagagaggtg aaatccatgt taatgatgct taagaaactc 750

ttgaaggcta tttgtgttgt ttttccacaa tgtgcgaaac tcagccatcc 800

ttagagaact gtggtgcctg tttcttttct ttttattttg aaggctcagg 850

agcatccata ggcatttgct ttttagaagt gtccactgca atggcaaaaa 900

tatttccagt tgcactgtat ctctggaagt gatgcatgaa ttcgattgga 950

ttgtgtcatt ttaaagtatt aaaaccaagg aaaccccaat tttgatgtat 1000

ggattacttt tttttgngcn cagggcc 1027

<210> 153
<211> 138
<212> PRT
<213> Homo sapiens

<220>
<221> N-myristoylation Sites
<222> 11-16, 51-56 and 116-121
<223> N-myristoylation Sites.

<220>
<221> Transmembrane domains
<222> 12-30, 33-52, 69-89 and 93-109
<223> Transmembrane domains

<220>
<221> Aminoacyl-transfer RNA Synthetases.
<222> 49-59
<223> Aminoacyl-transfer RNA synthetases class-II protein.

<400> 153

Met	Ile	Ser	Leu	Thr	Asp	Thr	Gln	Lys	Ile	Gly	Met	Gly	Leu	Thr	
1				5				10						15	
Gly	Phe	Gly	Val	Phe	Phe	Leu	Phe	Phe	Gly	Met	Ile	Leu	Phe	Phe	
				20				25						30	
Asp	Lys	Ala	Leu	Leu	Ala	Ile	Gly	Asn	Val	Leu	Phe	Val	Ala	Gly	
				35				40						45	
Leu	Ala	Phe	Val	Ile	Gly	Leu	Glu	Arg	Thr	Phe	Arg	Phe	Phe	Phe	
				50				55						60	

Gln Lys His Lys Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val
65 70 75

Phe Val Val Leu Ile Gly Trp Pro Leu Ile Gly Met Ile Phe Glu
80 85 90

Ile Tyr Gly Phe Phe Leu Leu Phe Arg Gly Phe Phe Pro Val Val
95 100 105

Val Gly Phe Ile Arg Arg Val Pro Val Leu Gly Ser Leu Leu Asn
110 115 120

Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val Gly Glu Ser Asn
125 130 135

Asn Met Val

<210> 154
<211> 405
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 66
<223> unknown base

<400> 154
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actcagcttc ccaccntggg ctttccgagg tgctttcgcc gctgtcccca 100

ccactgcagc catgatctcc ttaacggaca cgcagaaaat tggaatggga 150

ttaaccggat ttggagtgtt tttcctgttc tttggaatga ttctcttttt 200

tgacaaagca ctactggcta ttggaaatgt tttatttgta gccggcttgg 250

cttttgtaat tggtttagaa agaacattca gattcttctt ccaaaaacat 300

aaaatgaaag ctacaggttt ttttctgggt ggtgtatttg tagtccttat 350

tggttggcct ttgataggca tgatcttcga aatttatgga ttttttctct 400

tgttc 405

<210> 155
<211> 1781
<212> DNA
<213> Homo sapiens

<400> 155
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ccatgtgcca aaggctgcca ggaaggagac gccttcctga gtcctggatc 100

tttcttcctt ctggaaatct ttgactgtgg gtagttattt atttctgaat 150

aagagcgtcc acgcatcatg gacctcgcgg gactgctgaa gtctcagttc 200

ctgtgccacc tggtcttctg ctacgtcttt attgcctcag ggctaatcat 250

caacaccatt cagctcttca ctctcctcct ctggcccatt aacaagcagc 300

tcttccggaa gatcaactgc agactgtcct attgcatctc aagccagctg 350

gtgatgctgc tggagtggtg gtcgggcacg gaatgcacca tcttcacgga 400

cccgcgcgcc tacctcaagt atgggaagga aaatgccatc gtggttctca 450

accacaagtt tgaaattgac tttctgtgtg gctggagcct gtccgaacgc 500

tttgggctgt taggggctc caaggtcctg gccaagaaag agctggccta 550

tgtcccaatt atcggctgga tgtggtactt caccgagatg gtcttctgtt 600

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ctccgggact accccgagaa gtatttttc ctgattcact gtgagggcac 700

acggttcacg gagaagaagc atgagatcag catgcaggtg gcccgggcca 750

aggggctgcc tcgcctcaag catcacctgt tgccacgaac caagggcttc 800

gccatcaccg tgaggagctt gagaaatgta gtttcagctg tatatgactg 850

tacactcaat ttcagaaata atgaaaatcc aacactgctg ggagtcctaa 900

acggaaagaa ataccatgca gatttgtatg ttaggaggat cccactggaa 950

gacatccctg aagacgatga cgagtgctcg gcctggctgc acaagctcta 1000

ccaggagaag gatgcctttc aggaggagta ctacaggacg ggcaccttcc 1050

cagagacgcc catggtgccc ccccggcggc cctggaccct cgtgaactgg 1100

ctgttttggg cctcgctggt gctctaccct ttcttccagt tcctggtcag 1150

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tctttgtggc ctccgtggga gttcgatgga tgattggtgt gacggaaatt 1250

gacaagggct ctgcctacgg caactctgac agcaagcaga aactgaatga 1300

ctgactcagg gaggtgtcac catccgaagg gaaccttggg gaactggtgg 1350

cctctgcata tcctccttag tgggacacgg tgacaaaggc tgggtgagcc 1400

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atcctttggt gctgagtttt ctgtaaccct tggttgccag agataaagtg 1700

aaaagtgctt taggtgagat gactaaatta tgcctccaag aaaaaaaaat 1750

taaagtgctt ttctgggtca aaaaaaaaaa a 1781

<210> 156

<211> 378
<212> PRT
<213> Homo sapiens

<400> 156
Met Asp Leu Ala Gly Leu Leu Lys Ser Gln Phe Leu Cys His Leu
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Val Phe Cys Tyr Val Phe Ile Ala Ser Gly Leu Ile Ile Asn Thr
20 25 30

Ile Gln Leu Phe Thr Leu Leu Leu Trp Pro Ile Asn Lys Gln Leu
35 40 45

Phe Arg Lys Ile Asn Cys Arg Leu Ser Tyr Cys Ile Ser Ser Gln
50 55 60

Leu Val Met Leu Leu Glu Trp Trp Ser Gly Thr Glu Cys Thr Ile
65 70 75

Phe Thr Asp Pro Arg Ala Tyr Leu Lys Tyr Gly Lys Glu Asn Ala
80 85 90

Ile Val Val Leu Asn His Lys Phe Glu Ile Asp Phe Leu Cys Gly
95 100 105

Trp Ser Leu Ser Glu Arg Phe Gly Leu Leu Gly Gly Ser Lys Val
110 115 120

Leu Ala Lys Lys Glu Leu Ala Tyr Val Pro Ile Ile Gly Trp Met
125 130 135

Trp Tyr Phe Thr Glu Met Val Phe Cys Ser Arg Lys Trp Glu Gln
140 145 150

Asp Arg Lys Thr Val Ala Thr Ser Leu Gln His Leu Arg Asp Tyr
155 160 165

Pro Glu Lys Tyr Phe Phe Leu Ile His Cys Glu Gly Thr Arg Phe
170 175 180

Thr Glu Lys Lys His Glu Ile Ser Met Gln Val Ala Arg Ala Lys
185 190 195

Gly Leu Pro Arg Leu Lys His His Leu Leu Pro Arg Thr Lys Gly
200 205 210

Phe Ala Ile Thr Val Arg Ser Leu Arg Asn Val Val Ser Ala Val
215 220 225

Tyr Asp Cys Thr Leu Asn Phe Arg Asn Asn Glu Asn Pro Thr Leu
230 235 240

Leu Gly Val Leu Asn Gly Lys Lys Tyr His Ala Asp Leu Tyr Val
245 250 255

Arg Arg Ile Pro Leu Glu Asp Ile Pro Glu Asp Asp Asp Glu Cys
260 265 270

Ser Ala Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Phe Gln
275 280 285

Glu Glu Tyr Tyr Arg Thr Gly Thr Phe Pro Glu Thr Pro Met Val

290 295 300

Pro Pro Arg Arg Pro Trp Thr Leu Val Asn Trp Leu Phe Trp Ala
305 310 315

Ser Leu Val Leu Tyr Pro Phe Phe Gln Phe Leu Val Ser Met Ile
320 325 330

Arg Ser Gly Ser Ser Leu Thr Leu Ala Ser Phe Ile Leu Val Phe
335 340 345

Phe Val Ala Ser Val Gly Val Arg Trp Met Ile Gly Val Thr Glu
350 355 360

Ile Asp Lys Gly Ser Ala Tyr Gly Asn Ser Asp Ser Lys Gln Lys
365 370 375

Leu Asn Asp

<210> 157
<211> 1849
<212> DNA
<213> Homo sapiens

<400> 157
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gctttgtgct cggcgcactc gctttccagc acctcaacac ggactcggac 100

acggaaggtt ttcttcttgg ggaagtaaaa ggtgaagcca agaacagcat 150

tactgattcc caaatggatg atgttgaagt tgtttataca attgacattc 200

agaaatatat tccatgctat cagcttttta gcttttataa ttcttcaggc 250

gaagtaaatg agcaagcact gaagaaaata ttatcaaatg tcaaaaagaa 300

tgtggtaggt tggtacaaat tccgtcgtca ttcagatcag atcatgacgt 350

ttagagagag gctgcttcac aaaaacttgc aggagcattt ttcaaaccaa 400

gaccttgttt ttctgctatt aacaccaagt ataataacag aaagctgctc 450

tactcatcga ctggaacatt ccttatataa acctcaaaaa ggacttttc 500

acagggtacc tttagtggtt gccaatctgg gcatgtctga acaactgggt 550

tataaaactg tatcaggttc ctgtatgtcc actggtttta gccgagcagt 600

acaaacacac agctctaaat tttttgaaga agatggatcc ttaaaggagg 650

tacataagat aaatgaaatg tatgcttcat tacaagagga attaaagagt 700

atatgcaaaa aagtggaaga cagtgaacaa gcagtagata aactagtaaa 750

ggatgtaaac agattaaaac gagaaattga gaaaaggaga ggagcacaga 800

ttcaggcagc aagagagaag aacatccaaa aagaccctca ggagaacatt 850

tttctttgtc aggcattacg gacctttttt ccaaattctg aatttcttca 900

ttcatgtgtt atgtctttaa aaaatagaca tgtttctaaa agtagctgta 950

actacaacca ccatctcgat gtagtagaca atctgacctt aatggtagaa 1000

cacactgaca ttcctgaagc tagtccagct agtacaccac aaatcattaa 1050

gcataaagcc ttagacttag atgacagatg gcaattcaag agatctcggt 1100

tgttagatac acaagacaaa cgatctaaag caaatactgg tagtagtaac 1150

caagataaag catccaaaat gagcagccca gaaacagatg aagaaattga 1200

aaagatgaag ggttttggtg aatattcacg gtctcctaca ttttgatcct 1250

tttaacctta caaggagatt tttttatttg gctgatgggt aaagccaaac 1300

atttctattg tttttactat gttgagctac ttgcagtaag ttcatttgtt 1350

tttactatgt tcacctgttt gcagtaatac acagataact cttagtgcat 1400

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tcccagcact tagggaagac aagtcaggag gattgattga agctaggagt 1600

tagagaccag cctgggcaac gtattgagac catgtctatt aaaaaataaa 1650

atggaaaagc aagaatagcc ttattttcaa aatatggaaa gaaatttata 1700

tgaaaattta tctgagtcat taaaattctc cttaagtgat actttttag 1750

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aaatttgcaa aacatcatct aaaatttaaa aaaaaaaaaa aaaaaaaaa 1849

<210> 158
<211> 409
<212> PRT
<213> Homo sapiens

<400> 158

Met	Glu	Gly	Glu	Ser	Thr	Ser	Ala	Val	Leu	Ser	Gly	Phe	Val	Leu	
1				5				10					15		
Gly	Ala	Leu	Ala	Phe	Gln	His	Leu	Asn	Thr	Asp	Ser	Asp	Thr	Glu	
				20				25					30		
Gly	Phe	Leu	Leu	Gly	Glu	Val	Lys	Gly	Glu	Ala	Lys	Asn	Ser	Ile	
				35				40					45		
Thr	Asp	Ser	Gln	Met	Asp	Asp	Val	Glu	Val	Val	Tyr	Thr	Ile	Asp	
				50				55					60		
Ile	Gln	Lys	Tyr	Ile	Pro	Cys	Tyr	Gln	Leu	Phe	Ser	Phe	Tyr	Asn	
				65				70					75		
Ser	Ser	Gly	Glu	Val	Asn	Glu	Gln	Ala	Leu	Lys	Lys	Ile	Leu	Ser	
				80				85					90		
Asn	Val	Lys	Lys	Asn	Val	Val	Gly	Trp	Tyr	Lys	Phe	Arg	Arg	His	
				95				100					105		

Ser Asp Gln Ile Met Thr Phe Arg Glu Arg Leu Leu His Lys Asn
110 115 120

Leu Gln Glu His Phe Ser Asn Gln Asp Leu Val Phe Leu Leu Leu
125 130 135

Thr Pro Ser Ile Ile Thr Glu Ser Cys Ser Thr His Arg Leu Glu
140 145 150

His Ser Leu Tyr Lys Pro Gln Lys Gly Leu Phe His Arg Val Pro
155 160 165

Leu Val Val Ala Asn Leu Gly Met Ser Glu Gln Leu Gly Tyr Lys
170 175 180

Thr Val Ser Gly Ser Cys Met Ser Thr Gly Phe Ser Arg Ala Val
185 190 195

Gln Thr His Ser Ser Lys Phe Phe Glu Glu Asp Gly Ser Leu Lys
200 205 210

Glu Val His Lys Ile Asn Glu Met Tyr Ala Ser Leu Gln Glu Glu
215 220 225

Leu Lys Ser Ile Cys Lys Lys Val Glu Asp Ser Glu Gln Ala Val
230 235 240

Asp Lys Leu Val Lys Asp Val Asn Arg Leu Lys Arg Glu Ile Glu
245 250 255

Lys Arg Arg Gly Ala Gln Ile Gln Ala Ala Arg Glu Lys Asn Ile
260 265 270

Gln Lys Asp Pro Gln Glu Asn Ile Phe Leu Cys Gln Ala Leu Arg
275 280 285

Thr Phe Phe Pro Asn Ser Glu Phe Leu His Ser Cys Val Met Ser
290 295 300

Leu Lys Asn Arg His Val Ser Lys Ser Ser Cys Asn Tyr Asn His
305 310 315

His Leu Asp Val Val Asp Asn Leu Thr Leu Met Val Glu His Thr
320 325 330

Asp Ile Pro Glu Ala Ser Pro Ala Ser Thr Pro Gln Ile Ile Lys
335 340 345

His Lys Ala Leu Asp Leu Asp Asp Arg Trp Gln Phe Lys Arg Ser
350 355 360

Arg Leu Leu Asp Thr Gln Asp Lys Arg Ser Lys Ala Asn Thr Gly
365 370 375

Ser Ser Asn Gln Asp Lys Ala Ser Lys Met Ser Ser Pro Glu Thr
380 385 390

Asp Glu Glu Ile Glu Lys Met Lys Gly Phe Gly Glu Tyr Ser Arg
395 400 405

Ser Pro Thr Phe

<210> 159
<211> 2651
<212> DNA
<213> Homo sapiens

<400> 159
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ttccccgcgt ccccgcctcg ccggccagtc agcttgccgg gttcgctgcc 200

ccgcgaaacc ccgaggtcac cagcccgcgc ctctgcttcc ctgggccgcg 250

cgccgcctcc acgccctcct tctcccctgg cccggcgcct ggcaccgggg 300

accgttgcct gacgcgaggc ccagctctac ttttcgcccc gcgtctcctc 350

cgcctgctcg cctcttccac caactccaac tccttctccc tccagctcca 400

ctcgctagtc cccgactccg ccagccctcg gcccgctgcc gtagcgccgc 450

ttcccgtccg gtcccaaagg tgggaacgcg tccgccccgg cccgcaccat 500

ggcacggttc ggcttgcccg cgcttctctg caccctggca gtgctcagcg 550

ccgcgctgct ggctgccgag ctcaagtcga aaagttgctc ggaagtgcga 600

cgtctttacg tgtccaaagg cttcaacaag aacgatgccc ccctccacga 650

gatcaacggt gatcatttga agatctgtcc ccagggttct acctgctgct 700

ctcaagagat ggaggagaag tacagcctgc aaagtaaaga tgatttcaaa 750

agtgtggtca gcgaacagtg caatcatttg caagctgtct ttgcttcacg 800

ttacaagaag tttgatgaat tcttcaaaga actacttgaa aatgcagaga 850

aatccctgaa tgatatgttt gtgaagacat atggccattt atacatgcaa 900

aattctgagc tatttaaaga tctcttcgta gagttgaaac gttactacgt 950

ggtgggaaat gtgaacctgg aagaaatgct aaatgacttc tgggctcgcc 1000

tcctggagcg gatgttccgc ctggtgaact cccagtacca ctttacagat 1050

gagtatctgg aatgtgtgag caagtatacg gagcagctga agcccttcgg 1100

agatgtccct cgcaaattga agctccaggt tactcgtgct tttgtagcag 1150

cccgtacttt cgctcaaggc ttagcggttg cgggagatgt cgtgagcaag 1200

gtctccgtgg taaaccccac agcccagtgt acccatgccc tgttgaagat 1250

gatctactgc tcccactgcc ggggtctcgt gactgtgaag ccatgttaca 1300

actactgctc aaacatcatg agaggctgtt tggccaacca aggggatctc 1350

gattttgaat ggaacaattt catagatgct atgctgatgg tggcagagag 1400

gctagagggt cctttcaaca ttgaatcggt catggatccc atcgatgtga 1450

agatttctga tgctattatg aacatgcagg ataatagtgt tcaagtgtct 1500

cagaaggttt tccagggatg tggacccccc aagcccctcc cagctggacg 1550

aatttctcgt tccatctctg aaagtgcctt cagtgctcgc ttcagaccac 1600

atcaccccga ggaacgccca accacagcag ctggcactag tttggaccga 1650

ctggttactg atgtcaagga gaaactgaaa caggccaaga aattctggtc 1700

ctcccttccg agcaacgttt gcaacgatga gaggatggct gcaggaaacg 1750

gcaatgagga tgactgttgg aatgggaaag gcaaaagcag gtacctgttt 1800

gcagtgacag gaaatggatt agccaaccag ggcaacaacc cagaggtcca 1850

ggttgacacc agcaaaccag acatactgat ccttcgtcaa atcatggctc 1900

ttcgagtgat gaccagcaag atgaagaatg catacaatgg gaacgacgtg 1950

gacttctttg atatcagtga tgaaagtagt ggagaaggaa gtggaagtgg 2000

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ggggcacagg cctacctcct cactgtcttc tgcatcttgt tcctggttat 2150

gcagagagag tggagataat tctcaaactc tgagaaaaag tgttcatcaa 2200

aaagttaaaa ggcaccagtt atcacttttc taccatccta gtgactttgc 2250

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tttaagaagt gctgactttg ttttctcatt cagttttggg aggaaaaggg 2350

actgtgcatt gagttggttc ctgctccccc aaaccatgtt aaacgtggct 2400

aacagtgtag gtacagaact atagttagtt gtgcatttgt gattttatca 2450

ctctattatt tgtttgtatg ttttttttctc atttcgtttg tgggtttttt 2500

tttccaactg tgatctcgcc ttgtttctta caagcaaacc agggtccctt 2550

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c 2651

<210> 160
<211> 556
<212> PRT
<213> Homo sapiens

<400> 160

Met Ala Arg Phe Gly Leu Pro Ala Leu Leu Cys Thr Leu Ala Val
1 5 10 15

Leu Ser Ala Ala Leu Leu Ala Ala Glu Leu Lys Ser Lys Ser Cys
20 25 30

Ser Glu Val Arg Arg Leu Tyr Val Ser Lys Gly Phe Asn Lys Asn

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                35                  40                  45

Asp Ala Pro Leu His Glu Ile Asn Gly Asp His Leu Lys Ile Cys
                50                  55                  60

Pro Gln Gly Ser Thr Cys Cys Ser Gln Glu Met Glu Glu Lys Tyr
                65                  70                  75

Ser Leu Gln Ser Lys Asp Asp Phe Lys Ser Val Val Ser Glu Gln
                80                  85                  90

Cys Asn His Leu Gln Ala Val Phe Ala Ser Arg Tyr Lys Lys Phe
                95                 100                 105

Asp Glu Phe Phe Lys Glu Leu Leu Glu Asn Ala Glu Lys Ser Leu
               110                 115                 120

Asn Asp Met Phe Val Lys Thr Tyr Gly His Leu Tyr Met Gln Asn
               125                 130                 135

Ser Glu Leu Phe Lys Asp Leu Phe Val Glu Leu Lys Arg Tyr Tyr
               140                 145                 150

Val Val Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp
               155                 160                 165

Ala Arg Leu Leu Glu Arg Met Phe Arg Leu Val Asn Ser Gln Tyr
               170                 175                 180

His Phe Thr Asp Glu Tyr Leu Glu Cys Val Ser Lys Tyr Thr Glu
               185                 190                 195

Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Leu Gln
               200                 205                 210

Val Thr Arg Ala Phe Val Ala Ala Arg Thr Phe Ala Gln Gly Leu
               215                 220                 225

Ala Val Ala Gly Asp Val Val Ser Lys Val Ser Val Val Asn Pro
               230                 235                 240

Thr Ala Gln Cys Thr His Ala Leu Leu Lys Met Ile Tyr Cys Ser
               245                 250                 255

His Cys Arg Gly Leu Val Thr Val Lys Pro Cys Tyr Asn Tyr Cys
               260                 265                 270

Ser Asn Ile Met Arg Gly Cys Leu Ala Asn Gln Gly Asp Leu Asp
               275                 280                 285

Phe Glu Trp Asn Asn Phe Ile Asp Ala Met Leu Met Val Ala Glu
               290                 295                 300

Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile
               305                 310                 315

Asp Val Lys Ile Ser Asp Ala Ile Met Asn Met Gln Asp Asn Ser
               320                 325                 330

Val Gln Val Ser Gln Lys Val Phe Gln Gly Cys Gly Pro Pro Lys
               335                 340                 345

Pro Leu Pro Ala Gly Arg Ile Ser Arg Ser Ile Ser Glu Ser Ala
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                350                 355                 360

Phe Ser Ala Arg Phe Arg Pro His His Pro Glu Glu Arg Pro Thr
                365                 370                 375

Thr Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Val Lys
                380                 385                 390

Glu Lys Leu Lys Gln Ala Lys Lys Phe Trp Ser Ser Leu Pro Ser
                395                 400                 405

Asn Val Cys Asn Asp Glu Arg Met Ala Ala Gly Asn Gly Asn Glu
                410                 415                 420

Asp Asp Cys Trp Asn Gly Lys Gly Lys Ser Arg Tyr Leu Phe Ala
                425                 430                 435

Val Thr Gly Asn Gly Leu Ala Asn Gln Gly Asn Asn Pro Glu Val
                440                 445                 450

Gln Val Asp Thr Ser Lys Pro Asp Ile Leu Ile Leu Arg Gln Ile
                455                 460                 465

Met Ala Leu Arg Val Met Thr Ser Lys Met Lys Asn Ala Tyr Asn
                470                 475                 480

Gly Asn Asp Val Asp Phe Phe Asp Ile Ser Asp Glu Ser Ser Gly
                485                 490                 495

Glu Gly Ser Gly Ser Gly Cys Glu Tyr Gln Gln Cys Pro Ser Glu
                500                 505                 510

Phe Asp Tyr Asn Ala Thr Asp His Ala Gly Lys Ser Ala Asn Glu
                515                 520                 525

Lys Ala Asp Ser Ala Gly Val Arg Pro Gly Ala Gln Ala Tyr Leu
                530                 535                 540

Leu Thr Val Phe Cys Ile Leu Phe Leu Val Met Gln Arg Glu Trp
                545                 550                 555

Arg
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<210> 161
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 161
ctccgtggta aaccccacag ccc 23

<210> 162
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 162
tcacatcgat gggatccatg accg 24

<210> 163
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 163
ggtctcgtga ctgtgaagcc atgttacaac tactgctcaa acatcatgag 50

<210> 164
<211> 870
<212> DNA
<213> Homo sapiens

<400> 164
ctcgccctca aatgggaacg ctggcctggg actaaagcat agaccaccag 50

gctgagtatc ctgacctgag tcatccccag ggatcaggag cctccagcag 100

ggaaccttcc attatattct tcaagcaact tacagctgca ccgacagttg 150

cgatgaaagt tctaatctct tccctcctcc tgttgctgcc actaatgctg 200

atgtccatgg tctctagcag cctgaatcca ggggtcgcca gaggccacag 250

ggaccgaggc caggcttcta ggagatggct ccaggaaggc ggccaagaat 300

gtgagtgcaa agattggttc ctgagagccc cgagaagaaa attcatgaca 350

gtgtctgggc tgccaaagaa gcagtgcccc tgtgatcatt tcaagggcaa 400

tgtgaagaaa acaagacacc aaaggcacca cagaaagcca aacaagcatt 450

ccagagcctg ccagcaattt ctcaaacaat gtcagctaag aagctttgct 500

ctgcctttgt aggagctctg agcgcccact cttccaatta aacattctca 550

gccaagaaga cagtgagcac acctaccaga cactcttctt ctcccacctc 600

actctcccac tgtacccacc cctaaatcat tccagtgctc tcaaaaagca 650

tgtttttcaa gatcattttg tttgttgctc tctctagtgt cttcttctct 700

cgtcagtctt agcctgtgcc ctccccttac ccaggcttag gcttaattac 750

ctgaaagatt ccaggaaact gtagcttcct agctagtgtc atttaacctt 800

aaatgcaatc aggaaagtag caaacagaag tcaataaata tttttaaatg 850

tcaaaaaaaa aaaaaaaaaa 870

<210> 165
<211> 119
<212> PRT
<213> Homo sapiens

<400> 165
Met Lys Val Leu Ile Ser Ser Leu Leu Leu Leu Leu Pro Leu Met

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  1               5                  10                  15

Leu Met Ser Met Val Ser Ser Ser Leu Asn Pro Gly Val Ala Arg
                20                  25                  30

Gly His Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu
                35                  40                  45

Gly Gly Gln Glu Cys Glu Cys Lys Asp Trp Phe Leu Arg Ala Pro
                50                  55                  60

Arg Arg Lys Phe Met Thr Val Ser Gly Leu Pro Lys Lys Gln Cys
                65                  70                  75

Pro Cys Asp His Phe Lys Gly Asn Val Lys Lys Thr Arg His Gln
                80                  85                  90

Arg His His Arg Lys Pro Asn Lys His Ser Arg Ala Cys Gln Gln
                95                 100                 105

Phe Leu Lys Gln Cys Gln Leu Arg Ser Phe Ala Leu Pro Leu
               110                 115
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<210> 166
<211> 551
<212> DNA
<213> Homo sapiens

<400> 166
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tattcctgac ctgctatgca gacgacaaac cagacaagcc agacgacaag 100

ccagacgact cgggcaaaga cccaaagcca gacttcccca aattcctaag 150

cctcctgggc acagagatca ttgagaatgc agtcgagttc atcctccgct 200

ccatgtccag gagcacagga tttatggaat ttgatgataa tgaaggaaaa 250

cattcatcaa agtgacatcc tcaggacaca cccatgtggc tcctggacaa 300

tccaagagca gccaaatcct gcttttccag tttggctcca caagtcctcc 350

aggacagagc cctcaaagca actcccaacg agttctcagg attcaggctc 400

tggcttcaac caaacagaac tcattttgaa caccctgact gcatttttgc 450

ttttagaaag ttagaataaa tatggcgctt tgggatcaca tagttgatgg 500

agaggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 550

a 551

<210> 167
<211> 87
<212> PRT
<213> Homo sapiens

<400> 167
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Met Ala Val Leu Val Leu Arg Leu Thr Val Val Leu Gly Leu Leu
  1               5                  10                  15

Val Leu Phe Leu Thr Cys Tyr Ala Asp Asp Lys Pro Asp Lys Pro
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20 25 30

Asp Asp Lys Pro Asp Asp Ser Gly Lys Asp Pro Lys Pro Asp Phe
35 40 45

Pro Lys Phe Leu Ser Leu Leu Gly Thr Glu Ile Ile Glu Asn Ala
50 55 60

Val Glu Phe Ile Leu Arg Ser Met Ser Arg Ser Thr Gly Phe Met
65 70 75

Glu Phe Asp Asp Asn Glu Gly Lys His Ser Ser Lys
80 85

<210> 168
<211> 1371
<212> DNA
<213> Homo sapiens

<400> 168
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ggaagcacag ctcagagctg gtctgccatg gacatcctgg tcccactcct 100

gcagctgctg gtgctgcttc ttaccctgcc cctgcacctc atggctctgc 150

tgggctgctg gcagcccctg tgcaaaagct acttccccta cctgatggcc 200

gtgctgactc ccaagagcaa ccgcaagatg gagagcaaga aacgggagct 250

cttcagccag ataaaggggc ttacaggagc ctccgggaaa gtggccctac 300

tggagctggg ctgcggaacc ggagccaact ttcagttcta cccaccgggc 350

tgcagggtca cctgcctaga cccaaatccc cactttgaga agttcctgac 400

aaagagcatg gctgagaaca ggcacctcca atatgagcgg tttgtggtgg 450

ctcctggaga ggacatgaga cagctggctg atggctccat ggatgtggtg 500

gtctgcactc tggtgctgtg ctctgtgcag agcccaagga aggtcctgca 550

ggaggtccgg agagtactga gaccgggagg tgtgctcttt ttctgggagc 600

atgtggcaga accatatgga agctgggcct tcatgtggca gcaagttttc 650

gagcccacct ggaaacacat tggggatggc tgctgcctca ccagagagac 700

ctggaaggat cttgagaacg cccagttctc cgaaatccaa atggaacgac 750

agccccctcc cttgaagtgg ctacctgttg ggccccacat catgggaaag 800

gctgtcaaac aatctttccc aagctccaag gcactcattt gctccttccc 850

cagcctccaa ttagaacaag ccacccacca gcctatctat cttccactga 900

gagggaccta gcagaatgag agaagacatt catgtaccac ctactagtcc 950

ctctctcccc aacctctgcc agggcaatct ctaacttcaa tcccgccttc 1000

gacagtgaaa aagctctact tctacgctga cccagggagg aaacactagg 1050

accctgttgt atcctcaact gcaagtttct ggactagtct cccaacgttt 1100

gcctcccaat gttgtccctt tccttcgttc ccatggtaaa gctcctctcg 1150

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ccaccttctt cctgagctgg gggcaccagg gagaatcaga gatgctgggg 1300

atgccagagc aagactcaaa gaggcagagg ttttgttctc aaatattttt 1350

taataaatag acgaaaccac g 1371

<210> 169
<211> 277
<212> PRT
<213> Homo sapiens

<400> 169

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				20					25					30	
Leu	Cys	Lys	Ser	Tyr	Phe	Pro	Tyr	Leu	Met	Ala	Val	Leu	Thr	Pro	
				35					40					45	
Lys	Ser	Asn	Arg	Lys	Met	Glu	Ser	Lys	Lys	Arg	Glu	Leu	Phe	Ser	
				50					55					60	
Gln	Ile	Lys	Gly	Leu	Thr	Gly	Ala	Ser	Gly	Lys	Val	Ala	Leu	Leu	
				65					70					75	
Glu	Leu	Gly	Cys	Gly	Thr	Gly	Ala	Asn	Phe	Gln	Phe	Tyr	Pro	Pro	
				80					85					90	
Gly	Cys	Arg	Val	Thr	Cys	Leu	Asp	Pro	Asn	Pro	His	Phe	Glu	Lys	
				95					100					105	
Phe	Leu	Thr	Lys	Ser	Met	Ala	Glu	Asn	Arg	His	Leu	Gln	Tyr	Glu	
				110					115					120	
Arg	Phe	Val	Val	Ala	Pro	Gly	Glu	Asp	Met	Arg	Gln	Leu	Ala	Asp	
				125					130					135	
Gly	Ser	Met	Asp	Val	Val	Val	Cys	Thr	Leu	Val	Leu	Cys	Ser	Val	
				140					145					150	
Gln	Ser	Pro	Arg	Lys	Val	Leu	Gln	Glu	Val	Arg	Arg	Val	Leu	Arg	
				155					160					165	
Pro	Gly	Gly	Val	Leu	Phe	Phe	Trp	Glu	His	Val	Ala	Glu	Pro	Tyr	
				170					175					180	
Gly	Ser	Trp	Ala	Phe	Met	Trp	Gln	Gln	Val	Phe	Glu	Pro	Thr	Trp	
				185					190					195	
Lys	His	Ile	Gly	Asp	Gly	Cys	Cys	Leu	Thr	Arg	Glu	Thr	Trp	Lys	
				200					205					210	
Asp	Leu	Glu	Asn	Ala	Gln	Phe	Ser	Glu	Ile	Gln	Met	Glu	Arg	Gln	
				215					220					225	

Pro Pro Pro Leu Lys Trp Leu Pro Val Gly Pro His Ile Met Gly
230 235 240

Lys Ala Val Lys Gln Ser Phe Pro Ser Ser Lys Ala Leu Ile Cys
245 250 255

Ser Phe Pro Ser Leu Gln Leu Glu Gln Ala Thr His Gln Pro Ile
260 265 270

Tyr Leu Pro Leu Arg Gly Thr
275

<210> 170
<211> 1621
<212> DNA
<213> Homo sapiens

<400> 170
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cctcatcgca ggcagatgtt ggggctttgt ccgaacagct cccctctgcc 100

agcttctgta gataagggtt aaaaactaat atttatatga cagaagaaaa 150

agatgtcatt ccgtaaagta aacatcatca tcttggtcct ggctgttgct 200

ctcttcttac tggttttgca ccataacttc ctcagcttga gcagtttgtt 250

aaggaatgag gttacagatt caggaattgt agggcctcaa cctatagact 300

ttgtcccaaa tgctctccga catgcagtag atgggagaca agaggagatt 350

cctgtggtca tcgctgcatc tgaagacagg cttgggggggg ccattgcagc 400

tataaacagc attcagcaca acactcgctc caatgtgatt ttctacattg 450

ttactctcaa caatacagca gaccatctcc ggtcctggct caacagtgat 500

tccctgaaaa gcatcagata caaaattgtc aattttgacc ctaaactttt 550

ggaaggaaaa gtaaaggagg atcctgacca gggggaatcc atgaaacctt 600

taacctttgc aaggttctac ttgccaattc tggttcccag cgcaaagaag 650

gccatataca tggatgatga tgtaattgtg caaggtgata ttcttgccct 700

ttacaataca gcactgaagc caggacatgc agctgcattt tcagaagatt 750

gtgattcagc ctctactaaa gttgtcatcc gtggagcagg aaaccagtac 800

aattacattg gctatcttga ctataaaaag gaaagaattc gtaagctttc 850

catgaaagcc agcacttgct catttaatcc tggagttttt gttgcaaacc 900

tgacggaatg gaaacgacag aatataacta accaactgga aaaatggatg 950

aaactcaatg tagaagaggg actgtatagc agaaccctgg ctggtagcat 1000

cacaacacct cctctgctta tcgtatttta tcaacagcac tctaccatcg 1050

atcctatgtg gaatgtccgc caccttggtt ccagtgctgg aaaacgatat 1100

tcacctcagt ttgtaaaggc tgccaagtta ctccattgga atggacattt 1150

gaagccatgg ggaaggactg cttcatatac tgatgtttgg gaaaaatggt 1200

atattccaga cccaacaggc aaattcaacc taatccgaag atataccgag 1250

atctcaaaca taaagtgaaa cagaatttga actgtaagca agcatttctc 1300

aggaagtcct ggaagatagc atgcatggga agtaacagtt gctaggcttc 1350

aatgcctatc ggtagcaagc catggaaaaa gatgtgtcag ctaggtaaag 1400

atgacaaact gccctgtctg gcagtcagct tcccagacag actatagact 1450

ataaatatgt ctccatctgc cttaccaagt gttttcttac tacaatgctg 1500

aatgactgga aagaagaact gatatggcta gttcagctag ctggtacaga 1550

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taaataaaac ttacattttt c 1621

<210> 171
<211> 371
<212> PRT
<213> Homo sapiens

<400> 171

Met	Ser	Phe	Arg	Lys	Val	Asn	Ile	Ile	Ile	Leu	Val	Leu	Ala	Val	
1				5				10						15	
Ala	Leu	Phe	Leu	Leu	Val	Leu	His	His	Asn	Phe	Leu	Ser	Leu	Ser	
				20				25						30	
Ser	Leu	Leu	Arg	Asn	Glu	Val	Thr	Asp	Ser	Gly	Ile	Val	Gly	Pro	
				35				40						45	
Gln	Pro	Ile	Asp	Phe	Val	Pro	Asn	Ala	Leu	Arg	His	Ala	Val	Asp	
				50				55						60	
Gly	Arg	Gln	Glu	Glu	Ile	Pro	Val	Val	Ile	Ala	Ala	Ser	Glu	Asp	
				65				70						75	
Arg	Leu	Gly	Gly	Ala	Ile	Ala	Ala	Ile	Asn	Ser	Ile	Gln	His	Asn	
				80				85						90	
Thr	Arg	Ser	Asn	Val	Ile	Phe	Tyr	Ile	Val	Thr	Leu	Asn	Asn	Thr	
				95				100						105	
Ala	Asp	His	Leu	Arg	Ser	Trp	Leu	Asn	Ser	Asp	Ser	Leu	Lys	Ser	
				110				115						120	
Ile	Arg	Tyr	Lys	Ile	Val	Asn	Phe	Asp	Pro	Lys	Leu	Leu	Glu	Gly	
				125				130						135	
Lys	Val	Lys	Glu	Asp	Pro	Asp	Gln	Gly	Glu	Ser	Met	Lys	Pro	Leu	
				140				145						150	
Thr	Phe	Ala	Arg	Phe	Tyr	Leu	Pro	Ile	Leu	Val	Pro	Ser	Ala	Lys	
				155				160						165	
Lys	Ala	Ile	Tyr	Met	Asp	Asp	Asp	Val	Ile	Val	Gln	Gly	Asp	Ile	
				170				175						180	
Leu	Ala	Leu	Tyr	Asn	Thr	Ala	Leu	Lys	Pro	Gly	His	Ala	Ala	Ala	

185 190 195

Phe Ser Glu Asp Cys Asp Ser Ala Ser Thr Lys Val Val Ile Arg
200 205 210

Gly Ala Gly Asn Gln Tyr Asn Tyr Ile Gly Tyr Leu Asp Tyr Lys
215 220 225

Lys Glu Arg Ile Arg Lys Leu Ser Met Lys Ala Ser Thr Cys Ser
230 235 240

Phe Asn Pro Gly Val Phe Val Ala Asn Leu Thr Glu Trp Lys Arg
245 250 255

Gln Asn Ile Thr Asn Gln Leu Glu Lys Trp Met Lys Leu Asn Val
260 265 270

Glu Glu Gly Leu Tyr Ser Arg Thr Leu Ala Gly Ser Ile Thr Thr
275 280 285

Pro Pro Leu Leu Ile Val Phe Tyr Gln Gln His Ser Thr Ile Asp
290 295 300

Pro Met Trp Asn Val Arg His Leu Gly Ser Ser Ala Gly Lys Arg
305 310 315

Tyr Ser Pro Gln Phe Val Lys Ala Ala Lys Leu Leu His Trp Asn
320 325 330

Gly His Leu Lys Pro Trp Gly Arg Thr Ala Ser Tyr Thr Asp Val
335 340 345

Trp Glu Lys Trp Tyr Ile Pro Asp Pro Thr Gly Lys Phe Asn Leu
350 355 360

Ile Arg Arg Tyr Thr Glu Ile Ser Asn Ile Lys
365 370

<210> 172
<211> 585
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 71, 76, 86, 91, 162, 220, 269, 281
<223> unknown base

<400> 172
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aggttacaga ttcaggaatt ntaggncctc aacctntaga ntttgtccca 100

aatgttctcc gacatgcagt agatgggaga caagaggaga ttcctgtggt 150

catcgctgca tntgaagaca ggcttggggg ggccattgca gctataaaca 200

gcattcagca caacactcgn tccaatgtga ttttctacat tgttactctc 250

aacaatacag cagaccatnt ccggtcctgg ntcaacagtg attccctgaa 300

aagcatcaga tacaaaattg tcaattttga ccctaaactt ttggaaggaa 350

aagtaaagga ggatcctgac caggggaat ccatgaaacc tttaaccttt 400

gcaaggttct acttgccaat tctggttccc agcgcaaaga aggccatata 450

catggatgat gatgtaattg tgcaaggtga tattcttgcc ctttacaata 500

cagcactgaa gccaggacat gcagctgcat tttcagaaga ttgtgattca 550

gcctctacta aagttgtcat ccgtggagca ggaaa 585

<210> 173
<211> 1866
<212> DNA
<213> Homo sapiens

<400> 173
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gcggctgcca cggagctaga gggcaagtgt gctcggccca gcgtgcaggg 100

aacgcgggcg gccagacaac gggctgggct ccggggcctg cggcgcgggc 150

gctgagctgg cagggcgggt cggggcgcgg gctgcatccg catctcctcc 200

atcgcctgca gtaagggcgg ccgcggcgag cctttgaggg gaacgacttg 250

tcggagccct aaccaggggt gtctctgagc ctggtgggat ccccggagcg 300

tcacatcact ttccgatcac ttcaaagtgg ttaaaaacta atatttatat 350

gacagaagaa aaagatgtca ttccgtaaag taaacatcat catcttggtc 400

ctgggctgtt gctctcttct tactggtttt gcaccataac ttcctcagct 450

tgaggcagtt tgttaaggaa tgaggttaca gattcaggaa ttgtagggcc 500

tcaacctata ggactttgtc ccaaatgctc tccgacatgc agtagatggg 550

agacaagagg agattcctgt ggtcatcgct gcatctgaag acaggcttgg 600

gggggccatt gcagctataa acagcattca gcacaacact cgctccaatg 650

tgattttcta cattgttact ctcaacaata cagcagacca tctccggtcc 700

tgggctcaac agtgattccc tgaaaagcat cagatacaaa attgtcaatt 750

ttgaccctaa acttttggaa ggaaaagtaa aggaggatcc tgaccagggg 800

gaatccatga aacctttaac ctttgcaagg ttctacttgc caattctggg 850

ttcccagcgc aaagaaggcc atatacatgg atgatgatgt aattgtgcaa 900

ggtgatattc ttgcccttta caatacagca ctgaagccag gacatgcagc 950

tgcattttca gaagattgtg attcagcctc tactaaagtt gtcatccgtg 1000

gagcaggaaa ccagtacaat tacattggct atcttgacta taaaaaggaa 1050

agaattcgta agctttccat gaaagccagc acttgctcat ttaatcctgg 1100

agtttttgtt gcaaacctga cggaatggaa acgacagaat ataactaacc 1150

aactggaaaa atggatgaaa ctcaatgtag aagagggact gtatagcaga 1200

accctggctg gtagcatcac aacacctcct ctgcttatcg tattttatca 1250

acagcactct accatcgatc ctatgtggaa tgtccgccac cttggttcca 1300

gtgctggaaa acgatattca cctcagtttg taaaggctgc caagttactc 1350

cattggaatg gacatttgaa gccatgggga aggactgctt catatactga 1400

tgtttgggga aaaatggtat attccagacc caacaggcaa attcaaccta 1450

atccgaagat ataccgagat ctcaaacata aagtgaaaca gaatttgaac 1500

tgtaagcaag catttctcag gaagtcctgg aagatagcat gcgtgggaag 1550

taacagttgc taggcttcaa tgcctatcgg tagcaagcca tggaaaaaga 1600

tgtgtcagct aggtaaagat gacaaactgc cctgtctggc agtcagcttc 1650

ccagacagac tatagactat aaatatgtct ccatctgcct taccaagtgt 1700

tttcttacta caatgctgaa tgactggaaa gaagaactga tatggctagt 1750

tcagctagct ggtacagata attcaaaact gctgttggtt ttaattttgt 1800

aacctgtggc ctgatctgta aataaaactt acatttttca ataggtaaaa 1850

aaaaaaaaaa aaaaaa 1866

<210> 174
<211> 823
<212> DNA
<213> Homo sapiens

<400> 174
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acagcctcct ctgaaggccg gccataccag agtcctgcct cggcatgggc 100

ctcaccattg aggcagctcc actgtctgtg ctggtctgag ggtgctgcct 150

gtcatggggg cagccatctc ccaggggccc ctcatcgcca tcgtctgcaa 200

cggtctcgtg ggcttcttgc tgctgctgct ctgggtcatc ctctgctggg 250

cctgccattc tcgtctgccg acgttgactc tctctctgaa tccagtccca 300

actccagccc tggcccctgt cctgagaagg ccccaccacc ccagaagccc 350

agccatgaag gcagctacct gctgcagccc tgaaggcccc tggcctagcc 400

tggagcccag gacctaagtc cacctcacct agagcctgga attaggatcc 450

cagagttcag ccagcctggg gtccagaact caagagtccg cctgcttgga 500

gctggaccca gcggcccaga gtctagccag cttggctcca ataggagctc 550

agtggcccta aggagatggg cctggggtgg gggcttatga gttggtgcta 600

gagccagggc catctggact atgctccatc ccaagggcca agggtcaggg 650

gccgggtcca ctctttccct aggctgagca cctctaggcc ctctaggttg 700

gggaagcaaa ctggaaccca tggcaataat aggagggtgt ccaggctggg 750

ccccctcccct ggtcctccca gtgtttgctg gataataaat ggaactatgg 800

ctctaaaaaa aaaaaaaaaa aaa 823

<210> 175
<211> 87
<212> PRT
<213> Homo sapiens

<400> 175
Met Gly Ala Ala Ile Ser Gln Gly Ala Leu Ile Ala Ile Val Cys
1 5 10 15

Asn Gly Leu Val Gly Phe Leu Leu Leu Leu Leu Trp Val Ile Leu
20 25 30

Cys Trp Ala Cys His Ser Arg Leu Pro Thr Leu Thr Leu Ser Leu
35 40 45

Asn Pro Val Pro Thr Pro Ala Leu Ala Pro Val Leu Arg Arg Pro
50 55 60

His His Pro Arg Ser Pro Ala Met Lys Ala Ala Thr Cys Cys Ser
65 70 75

Pro Glu Gly Pro Trp Pro Ser Leu Glu Pro Arg Thr
80 85

<210> 176
<211> 1660
<212> DNA
<213> Homo sapiens

<400> 176
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cccaggctac cagttcctcc aagcaagtca tttcccttat ttaaccgatg 100

tgtccctcaa acacctgagt gctactccct atttgcatct gttttgataa 150

atgatgttga caccctccac cgaattctaa gtggaatcat gtcgggaaga 200

gatacaatcc ttggcctgtg tatcctcgca ttagccttgt ctttggccat 250

gatgtttacc ttcagattca tcaccaccct tctggttcac attttcattt 300

cattggttat tttgggattg ttgtttgtct gcggtgtttt atggtggctg 350

tattatgact ataccaacga cctcagcata gaattggaca cagaaaggga 400

aaatatgaag tgcgtgctgg ggtttgctat cgtatccaca ggcatcacgg 450

cagtgctgct cgtcttgatt tttgttctca gaaagagaat aaaattgaca 500

gttgagcttt tccaaatcac aaataaagcc atcagcagtg ctcccttcct 550

gctgttccag ccactgtgga catttgccat cctcattttc ttctgggtcc 600

tctgggtggc tgtgctgctg agcctgggaa ctgcaggagc tgcccaggtt 650

atggaaggcg gccaagtgga atataagccc ctttcgggca ttcggtacat 700

gtggtcgtac catttaattg gcctcatctg gactagtgaa ttcatccttg 750

cgtgccagca aatgactata gctggggcag tggttacttg ttatttcaac 800

agaagtaaaa atgatcctcc tgatcatccc atcctttcgt ctctctccat 850

tctcttcttc taccatcaag gaaccgttgt gaaagggtca tttttaatct 900

ctgtggtgag gattccgaga atcattgtca tgtacatgca aaacgcactg 950

aaagaacagc agcatggtgc attgtccagg tacctgttcc gatgctgcta 1000

ctgctgtttc tggtgtcttg acaaatacct gctccatctc aaccagaatg 1050

catatactac aactgctatt aatgggacag atttctgtac atcagcaaaa 1100

gatgcattca aaatcttgtc caagaactca agtcacttta catctattaa 1150

ctgctttgga gacttcataa tttttctagg aaaggtgtta gtggtgtgtt 1200

tcactgtttt tggaggactc atggctttta actacaatcg ggcattccag 1250

gtgtgggcag tccctctgtt attggtagct ttttttgcct acttagtagc 1300

ccatagtttt ttatctgtgt ttgaaactgt gctggatgca cttttcctgt 1350

gttttgctgt tgatctggaa acaaatgatg gatcgtcaga aaagccctac 1400

tttatggatc aagaatttct gagtttcgta aaaaggagca acaaattaaa 1450

caatgcaagg gcacagcagg acaagcactc attaaggaat gaggagggaa 1500

cagaactcca ggccattgtg agatagatac ccatttaggt atctgtacct 1550

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tagagaaaag ttagtgaatt ttttttaaa agacctaata aaccctattc 1650

ttcctcaaaa 1660

<210> 177
<211> 445
<212> PRT
<213> Homo sapiens

<400> 177

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Met Ser Gly Arg Asp Thr Ile Leu Gly Leu Cys Ile Leu Ala Leu
  1               5                  10                  15

Ala Leu Ser Leu Ala Met Met Phe Thr Phe Arg Phe Ile Thr Thr
             20                  25                  30

Leu Leu Val His Ile Phe Ile Ser Leu Val Ile Leu Gly Leu Leu
             35                  40                  45

Phe Val Cys Gly Val Leu Trp Trp Leu Tyr Tyr Asp Tyr Thr Asn
             50                  55                  60

Asp Leu Ser Ile Glu Leu Asp Thr Glu Arg Glu Asn Met Lys Cys
             65                  70                  75

Val Leu Gly Phe Ala Ile Val Ser Thr Gly Ile Thr Ala Val Leu
             80                  85                  90

Leu Val Leu Ile Phe Val Leu Arg Lys Arg Ile Lys Leu Thr Val
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95 100 105

Glu Leu Phe Gln Ile Thr Asn Lys Ala Ile Ser Ser Ala Pro Phe
110 115 120

Leu Leu Phe Gln Pro Leu Trp Thr Phe Ala Ile Leu Ile Phe Phe
125 130 135

Trp Val Leu Trp Val Ala Val Leu Leu Ser Leu Gly Thr Ala Gly
140 145 150

Ala Ala Gln Val Met Glu Gly Gly Gln Val Glu Tyr Lys Pro Leu
155 160 165

Ser Gly Ile Arg Tyr Met Trp Ser Tyr His Leu Ile Gly Leu Ile
170 175 180

Trp Thr Ser Glu Phe Ile Leu Ala Cys Gln Gln Met Thr Ile Ala
185 190 195

Gly Ala Val Val Thr Cys Tyr Phe Asn Arg Ser Lys Asn Asp Pro
200 205 210

Pro Asp His Pro Ile Leu Ser Ser Leu Ser Ile Leu Phe Phe Tyr
215 220 225

His Gln Gly Thr Val Val Lys Gly Ser Phe Leu Ile Ser Val Val
230 235 240

Arg Ile Pro Arg Ile Ile Val Met Tyr Met Gln Asn Ala Leu Lys
245 250 255

Glu Gln Gln His Gly Ala Leu Ser Arg Tyr Leu Phe Arg Cys Cys
260 265 270

Tyr Cys Cys Phe Trp Cys Leu Asp Lys Tyr Leu Leu His Leu Asn
275 280 285

Gln Asn Ala Tyr Thr Thr Thr Ala Ile Asn Gly Thr Asp Phe Cys
290 295 300

Thr Ser Ala Lys Asp Ala Phe Lys Ile Leu Ser Lys Asn Ser Ser
305 310 315

His Phe Thr Ser Ile Asn Cys Phe Gly Asp Phe Ile Ile Phe Leu
320 325 330

Gly Lys Val Leu Val Val Cys Phe Thr Val Phe Gly Gly Leu Met
335 340 345

Ala Phe Asn Tyr Asn Arg Ala Phe Gln Val Trp Ala Val Pro Leu
350 355 360

Leu Leu Val Ala Phe Phe Ala Tyr Leu Val Ala His Ser Phe Leu
365 370 375

Ser Val Phe Glu Thr Val Leu Asp Ala Leu Phe Leu Cys Phe Ala
380 385 390

Val Asp Leu Glu Thr Asn Asp Gly Ser Ser Glu Lys Pro Tyr Phe
395 400 405

Met Asp Gln Glu Phe Leu Ser Phe Val Lys Arg Ser Asn Lys Leu

410 415 420

Asn Asn Ala Arg Ala Gln Gln Asp Lys His Ser Leu Arg Asn Glu
425 430 435

Glu Gly Thr Glu Leu Gln Ala Ile Val Arg
440 445

<210> 178
<211> 2773
<212> DNA
<213> Homo sapiens

<400> 178
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tgtttcttcc ttagaataat ttgtatggga tttgtgatgc aggaaagcct 100

aagggaaaaa gaatattcat tctgtgtggt gaaaattttt tgaaaaaaaa 150

attgccttct tcaaacaagg gtgtcattct gatatttatg aggactgttg 200

ttctcactat gaaggcatct gttattgaaa tgttccttgt tttgctggtg 250

actggagtac attcaaacaa agaaacggca aagaagatta aaaggcccaa 300

gttcactgtg cctcagatca actgcgatgt caaagccgga aagatcatcg 350

atcctgagtt cattgtgaaa tgtccagcag gatgccaaga ccccaaatac 400

catgtttatg gcactgacgt gtatgcatcc tactccagtg tgtgtggcgc 450

tgccgtacac agtggtgtgc ttgataattc aggagggaaa atacttgttc 500

ggaaggttgc tggacagtct ggttacaaag ggagttattc caacggtgtc 550

caatcgttat ccctaccacg atggagagaa tcctttatcg tcttagaaag 600

taaacccaaa aagggtgtaa cctacccatc agctcttaca tactcatcat 650

cgaaaagtcc agctgcccaa gcaggtgaga ccacaaaagc ctatcagagg 700

ccacctattc cagggacaac tgcacagccg gtcactctga tgcagcttct 750

ggctgtcact gtagctgtgg ccacccccac caccttgcca aggccatccc 800

cttctgctgc ttctaccacc agcatcccca gaccacaatc agtgggccac 850

aggagccagg agatggatct ctggtccact gccacctaca caagcagcca 900

aaacaggccc agagctgatc caggtatcca aaggcaagat ccttcaggag 950

ctgccttcca gaaacctgtt ggagcggatg tcagcctggg acttgttcca 1000

aaagaagaat tgagcacaca gtctttggag ccagtatccc tgggagatcc 1050

aaactgcaaa attgacttgt cgtttttaat tgatgggagc accagcattg 1100

gcaaacggcg attccgaatc cagaagcagc tcctggctga tgttgcccaa 1150

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agacaaccct gctactcact ttaacctcaa gacacacacg aattctcgag 1250

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gtaggtcggg ccatctcctt tgtgaccaag aacttctttt ccaaagccaa 1350

tggaaacaga agcggggctc ccaatgtggt ggtggtgatg gtggatggct 1400

ggcccacgga caaagtggag gaggcttcaa gacttgcgag agagtcagga 1450

atcaacattt tcttcatcac cattgaaggt gctgctgaaa atgagaagca 1500

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gcttctactc gctccacgtg cagagctggt ttggcctcca caagaccctg 1600

cagcctctgg tgaagcgggt ctgcgacact gaccgcctgg cctgcagcaa 1650

gacctgcttg aactcggctg acattggctt cgtcatcgac ggctccagca 1700

gtgtggggac gggcaacttc cgcaccgtcc tccagtttgt gaccaacctc 1750

accaaagagt ttgagatttc cgacacggac acgcgcatcg gggccgtgca 1800

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agcctgacat cctcaacgcc atcaagaggg tgggctactg gagtggtggc 1900

accagcacgg gggctgccat caacttcgcc ctggagcagc tcttcaagaa 1950

gtccaagccc aacaagagga agttaatgat cctcatcacc gacgggaggt 2000

cctacgacga cgtccggatc ccagccatgg ctgcccatct gaagggagtg 2050

atcacctatg cgataggcgt tgcctgggct gcccaagagg agctagaagt 2100

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gggtgctgga gattttacat tttgacaatt gttttcaaaa taaatgttcg 2500

gaatacagtg cagcccttac gacaggctta cgtagagctt ttgtgagatt 2550

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aaaataaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2700

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aaaaaaaaaa aaaaaaaaaa aag 2773

<210> 179

<211> 678
<212> PRT
<213> Homo sapiens

<400> 179

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Met Arg Thr Val Val Leu Thr Met Lys Ala Ser Val Ile Glu Met
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Phe Leu Val Leu Leu Val Thr Gly Val His Ser Asn Lys Glu Thr
             20                  25                  30

Ala Lys Lys Ile Lys Arg Pro Lys Phe Thr Val Pro Gln Ile Asn
             35                  40                  45

Cys Asp Val Lys Ala Gly Lys Ile Ile Asp Pro Glu Phe Ile Val
             50                  55                  60

Lys Cys Pro Ala Gly Cys Gln Asp Pro Lys Tyr His Val Tyr Gly
             65                  70                  75

Thr Asp Val Tyr Ala Ser Tyr Ser Ser Val Cys Gly Ala Ala Val
             80                  85                  90

His Ser Gly Val Leu Asp Asn Ser Gly Gly Lys Ile Leu Val Arg
             95                 100                 105

Lys Val Ala Gly Gln Ser Gly Tyr Lys Gly Ser Tyr Ser Asn Gly
            110                 115                 120

Val Gln Ser Leu Ser Leu Pro Arg Trp Arg Glu Ser Phe Ile Val
            125                 130                 135

Leu Glu Ser Lys Pro Lys Lys Gly Val Thr Tyr Pro Ser Ala Leu
            140                 145                 150

Thr Tyr Ser Ser Ser Lys Ser Pro Ala Ala Gln Ala Gly Glu Thr
            155                 160                 165

Thr Lys Ala Tyr Gln Arg Pro Pro Ile Pro Gly Thr Thr Ala Gln
            170                 175                 180

Pro Val Thr Leu Met Gln Leu Leu Ala Val Thr Val Ala Val Ala
            185                 190                 195

Thr Pro Thr Thr Leu Pro Arg Pro Ser Pro Ser Ala Ala Ser Thr
            200                 205                 210

Thr Ser Ile Pro Arg Pro Gln Ser Val Gly His Arg Ser Gln Glu
            215                 220                 225

Met Asp Leu Trp Ser Thr Ala Thr Tyr Thr Ser Ser Gln Asn Arg
            230                 235                 240

Pro Arg Ala Asp Pro Gly Ile Gln Arg Gln Asp Pro Ser Gly Ala
            245                 250                 255

Ala Phe Gln Lys Pro Val Gly Ala Asp Val Ser Leu Gly Leu Val
            260                 265                 270

Pro Lys Glu Glu Leu Ser Thr Gln Ser Leu Glu Pro Val Ser Leu
            275                 280                 285

Gly Asp Pro Asn Cys Lys Ile Asp Leu Ser Phe Leu Ile Asp Gly
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290 295 300

Ser Thr Ser Ile Gly Lys Arg Arg Phe Arg Ile Gln Lys Gln Leu
305 310 315

Leu Ala Asp Val Ala Gln Ala Leu Asp Ile Gly Pro Ala Gly Pro
320 325 330

Leu Met Gly Val Val Gln Tyr Gly Asp Asn Pro Ala Thr His Phe
335 340 345

Asn Leu Lys Thr His Thr Asn Ser Arg Asp Leu Lys Thr Ala Ile
350 355 360

Glu Lys Ile Thr Gln Arg Gly Gly Leu Ser Asn Val Gly Arg Ala
365 370 375

Ile Ser Phe Val Thr Lys Asn Phe Phe Ser Lys Ala Asn Gly Asn
380 385 390

Arg Ser Gly Ala Pro Asn Val Val Val Val Met Val Asp Gly Trp
395 400 405

Pro Thr Asp Lys Val Glu Glu Ala Ser Arg Leu Ala Arg Glu Ser
410 415 420

Gly Ile Asn Ile Phe Phe Ile Thr Ile Glu Gly Ala Ala Glu Asn
425 430 435

Glu Lys Gln Tyr Val Val Glu Pro Asn Phe Ala Asn Lys Ala Val
440 445 450

Cys Arg Thr Asn Gly Phe Tyr Ser Leu His Val Gln Ser Trp Phe
455 460 465

Gly Leu His Lys Thr Leu Gln Pro Leu Val Lys Arg Val Cys Asp
470 475 480

Thr Asp Arg Leu Ala Cys Ser Lys Thr Cys Leu Asn Ser Ala Asp
485 490 495

Ile Gly Phe Val Ile Asp Gly Ser Ser Ser Val Gly Thr Gly Asn
500 505 510

Phe Arg Thr Val Leu Gln Phe Val Thr Asn Leu Thr Lys Glu Phe
515 520 525

Glu Ile Ser Asp Thr Asp Thr Arg Ile Gly Ala Val Gln Tyr Thr
530 535 540

Tyr Glu Gln Arg Leu Glu Phe Gly Phe Asp Lys Tyr Ser Ser Lys
545 550 555

Pro Asp Ile Leu Asn Ala Ile Lys Arg Val Gly Tyr Trp Ser Gly
560 565 570

Gly Thr Ser Thr Gly Ala Ala Ile Asn Phe Ala Leu Glu Gln Leu
575 580 585

Phe Lys Lys Ser Lys Pro Asn Lys Arg Lys Leu Met Ile Leu Ile
590 595 600

Thr Asp Gly Arg Ser Tyr Asp Asp Val Arg Ile Pro Ala Met Ala

605 610 615

Ala His Leu Lys Gly Val Ile Thr Tyr Ala Ile Gly Val Ala Trp
620 625 630

Ala Ala Gln Glu Glu Leu Glu Val Ile Ala Thr His Pro Ala Arg
635 640 645

Asp His Ser Phe Phe Val Asp Glu Phe Asp Asn Leu His Gln Tyr
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Val Pro Arg Ile Ile Gln Asn Ile Cys Thr Glu Phe Asn Ser Gln
665 670 675

Pro Arg Asn

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<211> 1759
<212> DNA
<213> Homo sapiens

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aacaaacatt cgagtggtag gaggactcct gtctgctcat ctgctctcca 350

agaaggctgg ggtggaagta gaggctggat ggccctgttc cgggcctctc 400

ctgagaatgg ctgaggaggc ggcccgaaaa ctcctcccag cctttcagac 450

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gaatttgcca ccctgagcag cctcactggt gacccggtgt tcgaagatgt 600

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tggtcggcaa ccacattgat gtgctcactg gcaagtgggt ggcccaggac 700

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agccatcctg cttcaggata agaagctcat ggccatgttc ctagagtata 800

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ctactggcct ggtcttcaga gcctcattgg agacattgac aatgccatga 950

ggaccttcct caactactac actgtatgga agcagtttgg ggggctcccg 1000

gaattctaca acattcctca gggatacaca gtggagaagc gagagggcta 1050

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cgggggatcc caccctccta gaactcggaa gagatgctgt ggaatccatt 1150

gaaaaaatca gcaaggtgga gtgcggattt gcaacaatca aagatctgcg 1200

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gggtccacct tcgacgcggt gatcaccccc tatggggagt gcatcctggg 1350

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atcataaaa 1759

<210> 181
<211> 541
<212> PRT
<213> Homo sapiens

<400> 181

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				20				25						30	
Asp	Pro	Ala	His	Tyr	Ser	Phe	Ser	Leu	Thr	Leu	Ile	Asp	Ala	Leu	
				35				40						45	
Asp	Thr	Leu	Leu	Ile	Leu	Gly	Asn	Val	Ser	Glu	Phe	Gln	Arg	Val	
				50				55						60	
Val	Glu	Val	Leu	Gln	Asp	Ser	Val	Asp	Phe	Asp	Ile	Asp	Val	Asn	
				65				70						75	
Ala	Ser	Val	Phe	Glu	Thr	Asn	Ile	Arg	Val	Val	Gly	Gly	Leu	Leu	
				80				85						90	
Ser	Ala	His	Leu	Leu	Ser	Lys	Lys	Ala	Gly	Val	Glu	Val	Glu	Ala	
				95				100						105	
Gly	Trp	Pro	Cys	Ser	Gly	Pro	Leu	Leu	Arg	Met	Ala	Glu	Glu	Ala	
				110				115						120	

Ala Arg Lys Leu Leu Pro Ala Phe Gln Thr Pro Thr Gly Met Pro

125 130 135

Tyr Gly Thr Val Asn Leu Leu His Gly Val Asn Pro Gly Glu Thr
140 145 150

Pro Val Thr Cys Thr Ala Gly Ile Gly Thr Phe Ile Val Glu Phe
155 160 165

Ala Thr Leu Ser Ser Leu Thr Gly Asp Pro Val Phe Glu Asp Val
170 175 180

Ala Arg Val Ala Leu Met Arg Leu Trp Glu Ser Arg Ser Asp Ile
185 190 195

Gly Leu Val Gly Asn His Ile Asp Val Leu Thr Gly Lys Trp Val
200 205 210

Ala Gln Asp Ala Gly Ile Gly Ala Gly Val Asp Ser Tyr Phe Glu
215 220 225

Tyr Leu Val Lys Gly Ala Ile Leu Leu Gln Asp Lys Lys Leu Met
230 235 240

Ala Met Phe Leu Glu Tyr Asn Lys Ala Ile Arg Asn Tyr Thr Arg
245 250 255

Phe Asp Asp Trp Tyr Leu Trp Val Gln Met Tyr Lys Gly Thr Val
260 265 270

Ser Met Pro Val Phe Gln Ser Leu Glu Ala Tyr Trp Pro Gly Leu
275 280 285

Gln Ser Leu Ile Gly Asp Ile Asp Asn Ala Met Arg Thr Phe Leu
290 295 300

Asn Tyr Tyr Thr Val Trp Lys Gln Phe Gly Gly Leu Pro Glu Phe
305 310 315

Tyr Asn Ile Pro Gln Gly Tyr Thr Val Glu Lys Arg Glu Gly Tyr
320 325 330

Pro Leu Arg Pro Glu Leu Ile Glu Ser Ala Met Tyr Leu Tyr Arg
335 340 345

Ala Thr Gly Asp Pro Thr Leu Leu Glu Leu Gly Arg Asp Ala Val
350 355 360

Glu Ser Ile Glu Lys Ile Ser Lys Val Glu Cys Gly Phe Ala Thr
365 370 375

Ile Lys Asp Leu Arg Asp His Lys Leu Asp Asn Arg Met Glu Ser
380 385 390

Phe Phe Leu Ala Glu Thr Val Lys Tyr Leu Tyr Leu Leu Phe Asp
395 400 405

Pro Thr Asn Phe Ile His Asn Asn Gly Ser Thr Phe Asp Ala Val
410 415 420

Ile Thr Pro Tyr Gly Glu Cys Ile Leu Gly Ala Gly Gly Tyr Ile
425 430 435

Phe Asn Thr Glu Ala His Pro Ile Asp Leu Ala Ala Leu His Cys

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                440                 445                 450

Cys Gln Arg Leu Lys Glu Glu Gln Trp Glu Val Glu Asp Leu Met
                455                 460                 465

Arg Glu Phe Tyr Ser Leu Lys Arg Ser Arg Ser Lys Phe Gln Lys
                470                 475                 480

Asn Thr Val Ser Ser Gly Pro Trp Glu Pro Pro Ala Arg Pro Gly
                485                 490                 495

Thr Leu Phe Ser Pro Glu Asn His Asp Gln Ala Arg Glu Arg Lys
                500                 505                 510

Pro Ala Lys Gln Lys Val Pro Leu Leu Ser Cys Pro Ser Gln Pro
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Phe Thr Ser Lys Leu Ala Leu Leu Gly Gln Val Phe Leu Asp Ser
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Ser
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<211> 2056
<212> DNA
<213> Homo sapiens

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tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200

gctttatttt ggaaagaaac aatgttctag gtcaaactga gtctaccaaa 250

tgcagacttt cacaatggtt ctagaagaaa tctggacaag tcttttcatg 300

tggtttttct acgcattgat tccatgtttg ctcacagatg aagtggccat 350

tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400

tcttgatgtg gagcccagtg atcgcgcctg gagaaacagt gtactattct 450

gtcgaatacc agggggagta cgagagcctg tacacgagcc acatctggat 500

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atgacatcac ggccactgtg ccatacaacc ttcgtgtcag ggccacattg 600

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acctggttat tgagctggag gacctggggc cccagtttga gttccttgtg 750

gcctactgga ggagggagcc tggtgccgag gaacatgtca aaatggtgag 800

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acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900

agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950

gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000

aattcagcaa ataaaaaggg ccaccctggc caaaagcggt aaaaaaaaaa 2050

aaaaaa 2056

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<212> PRT
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<221> Transmembrane domain
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            20                  25                  30

Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
            35                  40                  45

Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro
            50                  55                  60

Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu
            65                  70                  75

Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser
            80                  85                  90

Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala
            95                  100                 105

Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln
           110                 115                 120

Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser
           125                 130                 135

Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe
           140                 145                 150

His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe
           155                 160                 165

Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val
           170                 175                 180

Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met
           185                 190                 195

Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys
           200                 205                 210

Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu
           215                 220                 225
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Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe
230 235 240

Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp
245 250 255

Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val
260 265 270

Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile
275 280 285

Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met
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Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser
305 310

<210> 184
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<212> DNA
<213> Homo sapiens

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<223> unknown base

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tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150

agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200

ccaaatgcag actttcacaa tggttctaga agaaatctgg acaagtcttt 250

tcatgtggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300

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ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750

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tgacccac 808

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<211> 23
<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 185
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<210> 186
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<220>
<223> Synthetic oligonucleotide probe

<400> 186
ccaggtcggg taaggatggt tgag 24

<210> 187
<211> 50
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 187
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 188
<211> 1227
<212> DNA
<213> Homo sapiens

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gtgcggcttc acagaccagc actaccgagc cctgcagcag ctgcagcgag 250

acctgggccc ccaccacttt aacgtgctcg ccttcccctg caaccagttt 300

ggccaacagg agcctgacag caacaaggag attgagagct ttgcccgccg 350

cacctacagt gtctcattcc ccatgtttag caagattgca gtcaccggta 400

ctggtgccca tcctgccttc aagtacctgg cccagacttc tgggaaggag 450

cccacctgga acttctggaa gtacctagta gccccagatg gaaaggtggt 500

aggggcttgg gacccaactg tgtcagtgga ggaggtcaga ccccagatca 550

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taaaaatgaa agtatcctcc tcaaaaa 1227

<210> 189
<211> 187
<212> PRT
<213> Homo sapiens

<400> 189

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Ala	Ala	Cys	Ala	Gln	Gln	Glu	Gln	Asp	Phe	Tyr	Asp	Phe	Lys	Ala	
				20				25						30	
Val	Asn	Ile	Arg	Gly	Lys	Leu	Val	Ser	Leu	Glu	Lys	Tyr	Arg	Gly	
				35				40						45	
Ser	Val	Ser	Leu	Val	Val	Asn	Val	Ala	Ser	Glu	Cys	Gly	Phe	Thr	
				50				55						60	
Asp	Gln	His	Tyr	Arg	Ala	Leu	Gln	Gln	Leu	Gln	Arg	Asp	Leu	Gly	
				65				70						75	
Pro	His	His	Phe	Asn	Val	Leu	Ala	Phe	Pro	Cys	Asn	Gln	Phe	Gly	
				80				85						90	
Gln	Gln	Glu	Pro	Asp	Ser	Asn	Lys	Glu	Ile	Glu	Ser	Phe	Ala	Arg	
				95				100						105	
Arg	Thr	Tyr	Ser	Val	Ser	Phe	Pro	Met	Phe	Ser	Lys	Ile	Ala	Val	
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Thr	Gly	Thr	Gly	Ala	His	Pro	Ala	Phe	Lys	Tyr	Leu	Ala	Gln	Thr	
				125				130						135	
Ser	Gly	Lys	Glu	Pro	Thr	Trp	Asn	Phe	Trp	Lys	Tyr	Leu	Val	Ala	
				140				145						150	
Pro	Asp	Gly	Lys	Val	Val	Gly	Ala	Trp	Asp	Pro	Thr	Val	Ser	Val	

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Leu Leu Lys Arg Glu Asp Leu
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<210> 191
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<220>
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<400> 191
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<210> 192
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<211> 2187
<212> DNA
<213> Homo sapiens

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ctgggggccc gggccgccct ctctcggagt tggcaggaag ccaggttgca 150

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ctttatgcac ctagatgtcc ccagcaccca gttctgagcc aggcacatca 2000

aatgtcaagg aattgactga acgaactaag agctcctgga tgggtccggg 2050

aactcgcctg ggcacaaggt gccaaaaggc aggcagcctg cccaggccct 2100

ccctcctgtc catcccccac attcccctgt ctgtccttgt gatttggcat 2150

aaagagcttc tgttttcttt gaaaaaaaaa aaaaaaa 2187

<210> 194
<211> 615
<212> PRT
<213> Homo sapiens

<400> 194

Met	Ala	Val	Tyr	Val	Gly	Met	Leu	Arg	Leu	Gly	Arg	Leu	Cys	Ala	
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Gly	Ser	Ser	Gly	Val	Leu	Gly	Ala	Arg	Ala	Ala	Leu	Ser	Arg	Ser	
				20					25						30
Trp	Gln	Glu	Ala	Arg	Leu	Gln	Gly	Val	Arg	Phe	Leu	Ser	Ser	Arg	
				35					40						45
Glu	Val	Asp	Arg	Met	Val	Ser	Thr	Pro	Ile	Gly	Gly	Leu	Ser	Tyr	
				50					55						60
Val	Gln	Gly	Cys	Thr	Lys	Lys	His	Leu	Asn	Ser	Lys	Thr	Val	Gly	
				65					70						75
Gln	Cys	Leu	Glu	Thr	Thr	Ala	Gln	Arg	Val	Pro	Glu	Arg	Glu	Ala	
				80					85						90
Leu	Val	Val	Leu	His	Glu	Asp	Val	Arg	Leu	Thr	Phe	Ala	Gln	Leu	
				95					100						105
Lys	Glu	Glu	Val	Asp	Lys	Ala	Ala	Ser	Gly	Leu	Leu	Ser	Ile	Gly	
				110					115						120
Leu	Cys	Lys	Gly	Asp	Arg	Leu	Gly	Met	Trp	Gly	Pro	Asn	Ser	Tyr	
				125					130						135
Ala	Trp	Val	Leu	Met	Gln	Leu	Ala	Thr	Ala	Gln	Ala	Gly	Ile	Ile	
				140					145						150
Leu	Val	Ser	Val	Asn	Pro	Ala	Tyr	Gln	Ala	Met	Glu	Leu	Glu	Tyr	
				155					160						165
Val	Leu	Lys	Lys	Val	Gly	Cys	Lys	Ala	Leu	Val	Phe	Pro	Lys	Gln	
				170					175						180
Phe	Lys	Thr	Gln	Gln	Tyr	Tyr	Asn	Val	Leu	Lys	Gln	Ile	Cys	Pro	
				185					190						195
Glu	Val	Glu	Asn	Ala	Gln	Pro	Gly	Ala	Leu	Lys	Ser	Gln	Arg	Leu	
				200					205						210
Pro	Asp	Leu	Thr	Thr	Val	Ile	Ser	Val	Asp	Ala	Pro	Leu	Pro	Gly	
				215					220						225
Thr	Leu	Leu	Leu	Asp	Glu	Val	Val	Ala	Ala	Gly	Ser	Thr	Arg	Gln	
				230					235						240
His	Leu	Asp	Gln	Leu	Gln	Tyr	Asn	Gln	Gln	Phe	Leu	Ser	Cys	His	

245 250 255

Asp Pro Ile Asn Ile Gln Phe Thr Ser Gly Thr Thr Gly Ser Pro
260 265 270

Lys Gly Ala Thr Leu Ser His Tyr Asn Ile Val Asn Asn Ser Asn
275 280 285

Ile Leu Gly Glu Arg Leu Lys Leu His Glu Lys Thr Pro Glu Gln
290 295 300

Leu Arg Met Ile Leu Pro Asn Pro Leu Tyr His Cys Leu Gly Ser
305 310 315

Val Ala Gly Thr Met Met Cys Leu Met Tyr Gly Ala Thr Leu Ile
320 325 330

Leu Ala Ser Pro Ile Phe Asn Gly Lys Lys Ala Leu Glu Ala Ile
335 340 345

Ser Arg Glu Arg Gly Thr Phe Leu Tyr Gly Thr Pro Thr Met Phe
350 355 360

Val Asp Ile Leu Asn Gln Pro Asp Phe Ser Ser Tyr Asp Ile Ser
365 370 375

Thr Met Cys Gly Gly Val Ile Ala Gly Ser Pro Ala Pro Pro Glu
380 385 390

Leu Ile Arg Ala Ile Ile Asn Lys Ile Asn Met Lys Asp Leu Val
395 400 405

Val Ala Tyr Gly Thr Thr Glu Asn Ser Pro Val Thr Phe Ala His
410 415 420

Phe Pro Glu Asp Thr Val Glu Gln Lys Ala Glu Ser Val Gly Arg
425 430 435

Ile Met Pro His Thr Glu Ala Arg Ile Met Asn Met Glu Ala Gly
440 445 450

Thr Leu Ala Lys Leu Asn Thr Pro Gly Glu Leu Cys Ile Arg Gly
455 460 465

Tyr Cys Val Met Leu Gly Tyr Trp Gly Glu Pro Gln Lys Thr Glu
470 475 480

Glu Ala Val Asp Gln Asp Lys Trp Tyr Trp Thr Gly Asp Val Ala
485 490 495

Thr Met Asn Glu Gln Gly Phe Cys Lys Ile Val Gly Arg Ser Lys
500 505 510

Asp Met Ile Ile Arg Gly Gly Glu Asn Ile Tyr Pro Ala Glu Leu
515 520 525

Glu Asp Phe Phe His Thr His Pro Lys Val Gln Glu Val Gln Val
530 535 540

Val Gly Val Lys Asp Asp Arg Met Gly Glu Glu Ile Cys Ala Cys
545 550 555

Ile Arg Leu Lys Asp Gly Glu Glu Thr Thr Val Glu Glu Ile Lys

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560 565 570

Ala Phe Cys Lys Gly Lys Ile Ser His Phe Lys Ile Pro Lys Tyr
575 580 585

Ile Val Phe Val Thr Asn Tyr Pro Leu Thr Ile Ser Gly Lys Ile
590 595 600

Gln Lys Phe Lys Leu Arg Glu Gln Met Glu Arg His Leu Asn Leu
605 610 615

<210> 195
<211> 642
<212> DNA
<213> Homo sapiens

<400> 195
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agcagttgcg gatgatcctg cccaaccccc tgtaccattg cctgggttcc 100

gtggcaggca caatgatgtg tctgatgtac ggtgccaccc tcatcctggc 150

ctctcccatc ttcaatggca agaaggcact ggaggccatc agcagagaga 200

gaggcacctt cctgtatggt acccccacga tgttcgtgga cattctgaac 250

cagccagact tctccagtta tgacatctcg accatgtgtg gaggtgtcat 300

tgctgggtcc cctgcacctc cagagttgat ccgagccatc atcaacaaga 350

taaatatgaa ggacctggtg gttgcttatg gaaccacaga gaacagtccc 400

gtgacattcg cgcacttccc tgaggacact gtggagcaga aggcagaaag 450

cgtgggcaga attatgcctc acacggaggc gcggatcatg aacatggagg 500

cagggacgct ggcaaagctg aacacgcccg gggagctgtg catccgaggg 550

tactgcgtca tgctgggcta ctggggtgag cctcagaaga cagaggaagc 600

agtggatcag gacaagtggt attggacagg agatgtcgcc ac 642

<210> 196
<211> 1575
<212> DNA
<213> Homo sapiens

<400> 196
gagcaggacg gagccatgga ccccgccagg aaagcaggtg cccaggccat 50

gatctggact gcaggctggc tgctgctgct gctgcttcgc ggaggagcgc 100

aggccctgga gtgctacagc tgcgtgcaga aagcagatga cggatgctcc 150

ccgaacaaga tgaagacagt gaagtgcgcg ccgggcgtgg acgtctgcac 200

cgaggccgtg ggggcggtgg agaccatcca cggacaattc tcgctggcag 250

tgcggggttg cggttcggga ctccccggca agaatgaccg cggcctggat 300

cttcacgggc ttctggcgtt catccagctg cagcaatgcg ctcaggatcg 350

ctgcaacgcc aagctcaacc tcacctcgcg ggcgctcgac ccggcaggta 400

atgagagtgc atacccgccc aacggcgtgg agtgctacag ctgtgtgggc 450

ctgagccggg aggcgtgcca gggtacatcg ccgccggtcg tgagctgcta 500

caacgccagc gatcatgtct acaagggctg cttcgacggc aacgtcacct 550

tgacggcagc taatgtgact gtgtccttgc ctgtccgggg ctgtgtccag 600

gatgaattct gcactcggga tggagtaaca ggcccagggt tcacgctcag 650

tggctcctgt tgccaggggt cccgctgtaa ctctgacctc cgcaacaaga 700

cctacttctc ccctcgaatc ccacccctg tccggctgcc ccctccagag 750

cccacgactg tggcctcaac cacatctgtc accacttcta cctcggcccc 800

agtgagaccc acatccacca ccaaacccat gccagcgcca accagtcaga 850

ctccgagaca gggagtagaa cacgaggcct cccgggatga ggagcccagg 900

ttgactggag gcgccgctgg ccaccaggac cgcagcaatt cagggcagta 950

tcctgcaaaa ggggggcccc agcagcccca taataaaggc tgtgtggctc 1000

ccacagctgg attggcagcc cttctgttgg ccgtggctgc tggtgtccta 1050

ctgtgagctt ctccacctgg aaatttccct ctcacctact tctctggccc 1100

tgggtacccc tcttctcatc acttcctgtt cccaccactg gactgggctg 1150

gcccagcccc tgtttttcca acattcccca gtatccccag cttctgctgc 1200

gctggtttgc ggctttggga aataaaatac cgttgtatat attctgccag 1250

gggtgttcta gctttttgag gacagctcct gtatccttct catccttgtc 1300

tctccgcttg tcctcttgtg atgttaggac agagtgagag aagtcagctg 1350

tcacggggaa ggtgagagag aggatgctaa gcttcctact cactttctcc 1400

tagccagcct ggactttgga gcgtggggtg ggtgggacaa tggctcccca 1450

ctctaagcac tgcctccccc actccccgca tctttgggga atcggttccc 1500

catatgtctt ccttactaga ctgtgagctc ctcgaggggg ggcccggtac 1550

ccaattcgcc ctatagtgag tcgta 1575

<210> 197
<211> 346
<212> PRT
<213> Homo sapiens

<400> 197

Met	Asp	Pro	Ala	Arg	Lys	Ala	Gly	Ala	Gln	Ala	Met	Ile	Trp	Thr	
1				5				10						15	
Ala	Gly	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Arg	Gly	Gly	Ala	Gln	Ala	
				20				25						30	
Leu	Glu	Cys	Tyr	Ser	Cys	Val	Gln	Lys	Ala	Asp	Asp	Gly	Cys	Ser	

35 40 45

Pro Asn Lys Met Lys Thr Val Lys Cys Ala Pro Gly Val Asp Val
50 55 60

Cys Thr Glu Ala Val Gly Ala Val Glu Thr Ile His Gly Gln Phe
65 70 75

Ser Leu Ala Val Arg Gly Cys Gly Ser Gly Leu Pro Gly Lys Asn
80 85 90

Asp Arg Gly Leu Asp Leu His Gly Leu Leu Ala Phe Ile Gln Leu
95 100 105

Gln Gln Cys Ala Gln Asp Arg Cys Asn Ala Lys Leu Asn Leu Thr
110 115 120

Ser Arg Ala Leu Asp Pro Ala Gly Asn Glu Ser Ala Tyr Pro Pro
125 130 135

Asn Gly Val Glu Cys Tyr Ser Cys Val Gly Leu Ser Arg Glu Ala
140 145 150

Cys Gln Gly Thr Ser Pro Pro Val Val Ser Cys Tyr Asn Ala Ser
155 160 165

Asp His Val Tyr Lys Gly Cys Phe Asp Gly Asn Val Thr Leu Thr
170 175 180

Ala Ala Asn Val Thr Val Ser Leu Pro Val Arg Gly Cys Val Gln
185 190 195

Asp Glu Phe Cys Thr Arg Asp Gly Val Thr Gly Pro Gly Phe Thr
200 205 210

Leu Ser Gly Ser Cys Cys Gln Gly Ser Arg Cys Asn Ser Asp Leu
215 220 225

Arg Asn Lys Thr Tyr Phe Ser Pro Arg Ile Pro Pro Leu Val Arg
230 235 240

Leu Pro Pro Pro Glu Pro Thr Thr Val Ala Ser Thr Thr Ser Val
245 250 255

Thr Thr Ser Thr Ser Ala Pro Val Arg Pro Thr Ser Thr Thr Lys
260 265 270

Pro Met Pro Ala Pro Thr Ser Gln Thr Pro Arg Gln Gly Val Glu
275 280 285

His Glu Ala Ser Arg Asp Glu Glu Pro Arg Leu Thr Gly Gly Ala
290 295 300

Ala Gly His Gln Asp Arg Ser Asn Ser Gly Gln Tyr Pro Ala Lys
305 310 315

Gly Gly Pro Gln Gln Pro His Asn Lys Gly Cys Val Ala Pro Thr
320 325 330

Ala Gly Leu Ala Ala Leu Leu Leu Ala Val Ala Ala Gly Val Leu
335 340 345

Leu

<210> 198
<211> 1657
<212> DNA
<213> Homo sapiens

<400> 198
cgggactcgg cgggtcctcc tgggagtctc ggaggggacc ggctgtgcag 50

acgccatgga gttggtgctg gtcttcctct gcagcctgct ggcccccatg 100

gtcctggcca gtgcagctga aaaggagaag gaaatggacc cttttcatta 150

tgattaccag accctgagga ttgggggact ggtgttcgct gtggtcctct 200

tctcggttgg gatcctcctt atcctaagtc gcaggtgcaa gtgcagtttc 250

aatcagaagc cccgggcccc aggagatgag gaagcccagg tggagaacct 300

catcaccgcc aatgcaacag agccccagaa gcagagaact gaagtgcagc 350

catcaggtgg aagcctctgg aacctgaggc ggctgcttga acctttggat 400

gcaaatgtcg atgcttaaga aaaccggcca cttcagcaac agccctttcc 450

ccaggagaag ccaagaactt gtgtgtcccc caccctatcc cctctaacac 500

cattcctcca cctgatgatg caactaacac ttgcctcccc actgcagcct 550

gcggtcctgc ccacctcccg tgatgtgtgt gtgtgtgtgt gtgtgtgact 600

gtgtgtgttt gctaactgtg gtctttgtgg ctacttgttt gtggatggta 650

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cacatggcca tctgctcctc cctgcccccg tggccctcca tcaccttctg 750

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tgggaaggtt tgcagcactt tgtcatcatt cttcatggac tcctttcact 900

cctttaacaa aaaccttgct tccttatccc acctgatccc agtctgaagg 950

tctcttagca actggagata caaagcaagg agctggtgag cccagcgttg 1000

acgtcaggca ggctatgccc ttccgtggtt aatttcttcc caggggcttc 1050

cacgaggagt ccccatctgc cccgcccctt cacagagcgc ccggggattc 1100

caggcccagg gcttctactc tgcccctggg gaatgtgtcc cctgcatatc 1150

ttctcagcaa taactccatg ggctctggga ccctaccccc tccaaccttc 1200

cctgcttctg agacttcaat ctacagccca gctcatccag atgcagacta 1250

cagtccctgc aattgggtct ctggcaggca atagttgaag gactcctgtt 1300

ccgttggggc cagcacaccg ggatggatgg agggagagca gaggcctttg 1350

cttctctgcc tacgtcccct tagatgggca gcagaggcaa ctcccgcatc 1400

ctttgctctg cctgtcggtg gtcagagcgg tgagcgaggt gggttggaga 1450

ctcagcaggc tccgtgcagc ccttgggaac agtgagaggt tgaaggtcat 1500

aacgagagtg ggaactcaac ccagatcccg cccctcctgt cctctgtgtt 1550

cccgcggaaa ccaaccaaac cgtgcgctgt gacccattgc tgttctctgt 1600

atcgtgatct atcctcaaca acaacagaaa aaaggaataa aatatccttt 1650

gtttcct 1657

<210> 199
<211> 120
<212> PRT
<213> Homo sapiens

<400> 199

Met	Glu	Leu	Val	Leu	Val	Phe	Leu	Cys	Ser	Leu	Leu	Ala	Pro	Met	
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Val	Leu	Ala	Ser	Ala	Ala	Glu	Lys	Glu	Lys	Glu	Met	Asp	Pro	Phe	
			20					25						30	
His	Tyr	Asp	Tyr	Gln	Thr	Leu	Arg	Ile	Gly	Gly	Leu	Val	Phe	Ala	
			35					40						45	
Val	Val	Leu	Phe	Ser	Val	Gly	Ile	Leu	Leu	Ile	Leu	Ser	Arg	Arg	
			50					55						60	
Cys	Lys	Cys	Ser	Phe	Asn	Gln	Lys	Pro	Arg	Ala	Pro	Gly	Asp	Glu	
			65					70						75	
Glu	Ala	Gln	Val	Glu	Asn	Leu	Ile	Thr	Ala	Asn	Ala	Thr	Glu	Pro	
			80					85						90	
Gln	Lys	Gln	Arg	Thr	Glu	Val	Gln	Pro	Ser	Gly	Gly	Ser	Leu	Trp	
			95					100						105	
Asn	Leu	Arg	Arg	Leu	Leu	Glu	Pro	Leu	Asp	Ala	Asn	Val	Asp	Ala	
			110					115						120	

<210> 200
<211> 415
<212> DNA
<213> Homo sapiens

<400> 200
aaacttgacg ccatgaagat cccggtcctt cctgccgtgg tgctcctctc 50

cctcctggtg ctccactctg cccagggagc caccctgggt ggtcctgagg 100

aagaaagcac cattgagaat tatgcgtcac gacccgaggc ctttaacacc 150

ccgttcctga acatcgacaa attgcgatct gcgtttaagg ctgatgagtt 200

cctgaactgg cacgccctct ttgagtctat caaaaggaaa cttcctttcc 250

tcaactggga tgcctttcct aagctgaaag gactgaggag cgcaactcct 300

gatgcccagt gaccatgacc tccactggaa gaggggggcta gcgtgagcgc 350

tgattctcaa cctaccataa ctctttcctg cctcaggaac tccaataaaa 400

catttttccat ccaaa 415

<210> 201
<211> 99
<212> PRT
<213> Homo sapiens

<400> 201
Met Lys Ile Pro Val Leu Pro Ala Val Val Leu Leu Ser Leu Leu
1 5 10 15

Val Leu His Ser Ala Gln Gly Ala Thr Leu Gly Gly Pro Glu Glu
20 25 30

Glu Ser Thr Ile Glu Asn Tyr Ala Ser Arg Pro Glu Ala Phe Asn
35 40 45

Thr Pro Phe Leu Asn Ile Asp Lys Leu Arg Ser Ala Phe Lys Ala
50 55 60

Asp Glu Phe Leu Asn Trp His Ala Leu Phe Glu Ser Ile Lys Arg
65 70 75

Lys Leu Pro Phe Leu Asn Trp Asp Ala Phe Pro Lys Leu Lys Gly
80 85 90

Leu Arg Ser Ala Thr Pro Asp Ala Gln
95

<210> 202
<211> 678
<212> DNA
<213> Homo sapiens

<400> 202
cagttctgaa atcaatggag ttaatttagg gaatacaaac cagccatggg 50

ggtggagatt gcctttgcct cagtgattct cacctgcctc tcccttctgg 100

cagcaggagt ctcccaggtt gttcttctcc agccagttcc aactcaggag 150

acaggtccca aggccatggg agatctctcc tgtggctttg ccggccactc 200

atgagagtgt ttttgtgtaa agtatttttt agaatactgt tgacttcttc 250

atgatttaat aaccatcctt tgcgaagttt tatgaggctt taggggaatg 300

tcaaccctca aatttttgtt atactagatg gcttccattt acccaccact 350

attttaaggt ccctttattt ttaggttcaa ggttcatttg acttgagaaa 400

gtgcccttct gcagcttcat tgattttgtt tatcttcact attaattgta 450

acgattaaaa aagaataaga gcacgcagac ctctaggaga tatttttatc 500

cctgggtgcc cctgacacat ttatgtagtg atcccacaaa tgtgattgtt 550

aatttaaatg ttattctaat attagtacat tcagttgtga tgtaatatga 600

ataaccagaa tctatttctt aaaagttttg agtatatttt tcaactagat 650

atttgtatag aaagactgaa tagtgatg 678

<210> 203
<211> 52
<212> PRT
<213> Homo sapiens

<400> 203
Met Gly Val Glu Ile Ala Phe Ala Ser Val Ile Leu Thr Cys Leu
1 5 10 15

Ser Leu Leu Ala Ala Gly Val Ser Gln Val Val Leu Leu Gln Pro
20 25 30

Val Pro Thr Gln Glu Thr Gly Pro Lys Ala Met Gly Asp Leu Ser
35 40 45

Cys Gly Phe Ala Gly His Ser
50

<210> 204
<211> 1917
<212> DNA
<213> Homo sapiens

<400> 204
ggggaatctg cagtaggtct gccggcgatg gagtggtggg ctagctcgcc 50

gcttcggctc tggctgctgt tgttcctcct gccctcagcg cagggccgcc 100

agaaggagtc aggttcaaaa tggaaagtat ttattgacca aattaacagg 150

tctttggaga attacgaacc atgttcaagt caaaactgca gctgctacca 200

tggtgtcata gaagaggatc taactccttt ccgaggaggc atctccagga 250

agatgatggc agaggtagtc agacggaagc tagggaccca ctatcagatc 300

actaagaaca gactgtaccg ggaaaatgac tgcatgttcc cctcaaggtg 350

tagtggtgtt gagcacttta ttttggaagt gatcgggcgt ctccctgaca 400

tggagatggt gatcaatgta cgagattatc ctcaggttcc taaatggatg 450

gagcctgcca tcccagtctt ctccttcagt aagacatcag agtaccatga 500

tatcatgtat cctgcttgga cattttggga agggggacct gctgtttggc 550

caatttatcc tacaggtctt ggacggtggg acctcttcag agaagatctg 600

gtaaggtcag cagcacagtg gccatggaaa aagaaaaact ctacagcata 650

tttccgagga tcaaggacaa gtccagaacg agatcctctc attcttctgt 700

ctcggaaaaa cccaaaactt gttgatgcag aatacaccaa aaaccaggcc 750

tggaaatcta tgaaagatac cttaggaaag ccagctgcta aggatgtcca 800

tcttgtggat cactgcaaat acaagtatct gtttaatttt cgaggcgtag 850

ctgcaagttt ccggtttaaa cacctcttcc tgtgtggctc acttgttttc 900

catgttggtg atgagtggct agaattcttc tatccacagc tgaagccatg 950

ggttcactat atcccagtca aaacagatct ctccaatgtc caagagctgt 1000

tacaatttgt aaaagcaaat gatgatgtag ctcaagagat tgctgaaagg 1050

ggaagccagt ttattaggaa ccatttgcag atggatgaca tcacctgtta 1100

ctgggagaac ctcttgagtg aatactctaa attcctgtct tataatgtaa 1150

cgagaaggaa aggttatgat caaattattc ccaaaatgtt gaaaactgaa 1200

ctatagtagt catcatagga ccatagtcct ctttgtggca acagatctca 1250

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agttcaactt tttggatgaa taaggaccag aaatcgtgag atgtggattt 1450

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tgtgatgatg ccctttgtcc cattatttgg agcagaaaat tcgtcatttg 1600

gaagtagtac aactcattgc tggaattgtg aaattattca aggcgtgatc 1650

tctgtcactt tattttaatg taggaaaccc tatggggttt atgaaaaata 1700

cttggggatc attctctgaa tggtctaagg aagcggtagc catgccatgc 1750

aatgatgtag gagttctctt ttgtaaaacc ataaactctg ttactcagga 1800

ggtttctata atgccacata gaaagaggcc aattgcatga gtaattattg 1850

caattggatt tcaggttccc tttttgtgcc ttcatgccct acttcttaat 1900

gcctctctaa agccaaa 1917

<210> 205
<211> 392
<212> PRT
<213> Homo sapiens

<400> 205

Met	Glu	Trp	Trp	Ala	Ser	Ser	Pro	Leu	Arg	Leu	Trp	Leu	Leu	Leu	
1				5				10						15	
Phe	Leu	Leu	Pro	Ser	Ala	Gln	Gly	Arg	Gln	Lys	Glu	Ser	Gly	Ser	
				20				25						30	
Lys	Trp	Lys	Val	Phe	Ile	Asp	Gln	Ile	Asn	Arg	Ser	Leu	Glu	Asn	
				35				40						45	
Tyr	Glu	Pro	Cys	Ser	Ser	Gln	Asn	Cys	Ser	Cys	Tyr	His	Gly	Val	
				50				55						60	
Ile	Glu	Glu	Asp	Leu	Thr	Pro	Phe	Arg	Gly	Gly	Ile	Ser	Arg	Lys	
				65				70						75	
Met	Met	Ala	Glu	Val	Val	Arg	Arg	Lys	Leu	Gly	Thr	His	Tyr	Gln	
				80				85						90	

Ile Thr Lys Asn Arg Leu Tyr Arg Glu Asn Asp Cys Met Phe Pro

95 100 105

Ser Arg Cys Ser Gly Val Glu His Phe Ile Leu Glu Val Ile Gly
110 115 120

Arg Leu Pro Asp Met Glu Met Val Ile Asn Val Arg Asp Tyr Pro
125 130 135

Gln Val Pro Lys Trp Met Glu Pro Ala Ile Pro Val Phe Ser Phe
140 145 150

Ser Lys Thr Ser Glu Tyr His Asp Ile Met Tyr Pro Ala Trp Thr
155 160 165

Phe Trp Glu Gly Gly Pro Ala Val Trp Pro Ile Tyr Pro Thr Gly
170 175 180

Leu Gly Arg Trp Asp Leu Phe Arg Glu Asp Leu Val Arg Ser Ala
185 190 195

Ala Gln Trp Pro Trp Lys Lys Lys Asn Ser Thr Ala Tyr Phe Arg
200 205 210

Gly Ser Arg Thr Ser Pro Glu Arg Asp Pro Leu Ile Leu Leu Ser
215 220 225

Arg Lys Asn Pro Lys Leu Val Asp Ala Glu Tyr Thr Lys Asn Gln
230 235 240

Ala Trp Lys Ser Met Lys Asp Thr Leu Gly Lys Pro Ala Ala Lys
245 250 255

Asp Val His Leu Val Asp His Cys Lys Tyr Lys Tyr Leu Phe Asn
260 265 270

Phe Arg Gly Val Ala Ala Ser Phe Arg Phe Lys His Leu Phe Leu
275 280 285

Cys Gly Ser Leu Val Phe His Val Gly Asp Glu Trp Leu Glu Phe
290 295 300

Phe Tyr Pro Gln Leu Lys Pro Trp Val His Tyr Ile Pro Val Lys
305 310 315

Thr Asp Leu Ser Asn Val Gln Glu Leu Leu Gln Phe Val Lys Ala
320 325 330

Asn Asp Asp Val Ala Gln Glu Ile Ala Glu Arg Gly Ser Gln Phe
335 340 345

Ile Arg Asn His Leu Gln Met Asp Asp Ile Thr Cys Tyr Trp Glu
350 355 360

Asn Leu Leu Ser Glu Tyr Ser Lys Phe Leu Ser Tyr Asn Val Thr
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Arg Arg Lys Gly Tyr Asp Gln Ile Ile Pro Lys Met Leu Lys Thr
380 385 390

Glu Leu

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<211> 1425
<212> DNA
<213> Homo sapiens

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ccccctggc atgggatctg gggctcctgc ttctatttgt tgggcagcac 250

agcctcatgg cagctgaaag agtgaaggca tggacatccc ggtactttgg 300

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ctgggctcag accccaacct agtcaagggg attctcctgc tcttaactcg 1350

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<211> 262
<212> PRT
<213> Homo sapiens

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Leu Arg Pro Leu Leu Gly Gly Ile Pro Glu Ser Gly Gly Pro Asp
35 40 45

Ala Arg Gln Gly Trp Leu Ala Ala Leu Gln Asp Arg Ser Ile Leu
50 55 60

Ala Pro Leu Ala Trp Asp Leu Gly Leu Leu Leu Leu Phe Val Gly
65 70 75

Gln His Ser Leu Met Ala Ala Glu Arg Val Lys Ala Trp Thr Ser
80 85 90

Arg Tyr Phe Gly Val Leu Gln Arg Ser Leu Tyr Val Ala Cys Thr
95 100 105

Ala Leu Ala Leu Gln Leu Val Met Arg Tyr Trp Glu Pro Ile Pro
110 115 120

Lys Gly Pro Val Leu Trp Glu Ala Arg Ala Glu Pro Trp Ala Thr
125 130 135

Trp Val Pro Leu Leu Cys Phe Val Leu His Val Ile Ser Trp Leu
140 145 150

Leu Ile Phe Ser Ile Leu Leu Val Phe Asp Tyr Ala Glu Leu Met
155 160 165

Gly Leu Lys Gln Val Tyr Tyr His Val Leu Gly Leu Gly Glu Pro
170 175 180

Leu Ala Leu Lys Ser Pro Arg Ala Leu Arg Leu Phe Ser His Leu
185 190 195

Arg His Pro Val Cys Val Glu Leu Leu Thr Val Leu Trp Val Val
200 205 210

Pro Thr Leu Gly Thr Asp Arg Leu Leu Leu Ala Phe Leu Leu Thr
215 220 225

Leu Tyr Leu Gly Leu Ala His Gly Leu Asp Gln Gln Asp Leu Arg
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Tyr Leu Arg Ala Gln Leu Gln Arg Lys Leu His Leu Leu Ser Arg
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Pro Gln Asp Gly Glu Ala Glu
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<211> 2095
<212> DNA

<213> Homo sapiens

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caacaaaaaa cttaagcttt aatttcatct ggaattccac agttttctta 200

gctccctgga cccggttgac ctgttggctc ttcccgctgg ctgctctatc 250

acgtggtgct ctccgactac tcaccccgag tgtaaagaac cttcggctcg 300

cgtgcttctg agctgctgtg gatggcctcg gctctctgga ctgtccttcc 350

gagtaggatg tcactgagat ccctcaaatg gagcctcctg ctgctgtcac 400

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tactgtggta atatagagaa gaattaaagc aagaaaatct gaaaa 2095

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<212> PRT
<213> Homo sapiens

<400> 209

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				20				25						30
Phe	Val	Met	Trp	Tyr	Leu	Ser	Leu	Pro	His	Tyr	Asn	Val	Ile	Glu
				35				40						45
Arg	Val	Asn	Trp	Met	Tyr	Phe	Tyr	Glu	Tyr	Glu	Pro	Ile	Tyr	Arg
				50				55						60
Gln	Asp	Phe	His	Phe	Thr	Leu	Arg	Glu	His	Ser	Asn	Cys	Ser	His
				65				70						75
Gln	Asn	Pro	Phe	Leu	Val	Ile	Leu	Val	Thr	Ser	His	Pro	Ser	Asp
				80				85						90
Val	Lys	Ala	Arg	Gln	Ala	Ile	Arg	Val	Thr	Trp	Gly	Glu	Lys	Lys
				95				100						105
Ser	Trp	Trp	Gly	Tyr	Glu	Val	Leu	Thr	Phe	Phe	Leu	Leu	Gly	Gln
				110				115						120
Glu	Ala	Glu	Lys	Glu	Asp	Lys	Met	Leu	Ala	Leu	Ser	Leu	Glu	Asp
				125				130						135
Glu	His	Leu	Leu	Tyr	Gly	Asp	Ile	Ile	Arg	Gln	Asp	Phe	Leu	Asp
				140				145						150
Thr	Tyr	Asn	Asn	Leu	Thr	Leu	Lys	Thr	Ile	Met	Ala	Phe	Arg	Trp
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Val Thr Glu Phe Cys Pro Asn Ala Lys Tyr Val Met Lys Thr Asp
170 175 180

Thr Asp Val Phe Ile Asn Thr Gly Asn Leu Val Lys Tyr Leu Leu
185 190 195

Asn Leu Asn His Ser Glu Lys Phe Phe Thr Gly Tyr Pro Leu Ile
200 205 210

Asp Asn Tyr Ser Tyr Arg Gly Phe Tyr Gln Lys Thr His Ile Ser
215 220 225

Tyr Gln Glu Tyr Pro Phe Lys Val Phe Pro Pro Tyr Cys Ser Gly
230 235 240

Leu Gly Tyr Ile Met Ser Arg Asp Leu Val Pro Arg Ile Tyr Glu
245 250 255

Met Met Gly His Val Lys Pro Ile Lys Phe Glu Asp Val Tyr Val
260 265 270

Gly Ile Cys Leu Asn Leu Leu Lys Val Asn Ile His Ile Pro Glu
275 280 285

Asp Thr Asn Leu Phe Phe Leu Tyr Arg Ile His Leu Asp Val Cys
290 295 300

Gln Leu Arg Arg Val Ile Ala Ala His Gly Phe Ser Ser Lys Glu
305 310 315

Ile Ile Thr Phe Trp Gln Val Met Leu Arg Asn Thr Thr Cys His
320 325 330

Tyr

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<211> 745
<212> DNA
<213> Homo sapiens

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gtgtcaacaa tgaacacaat gtggccaatg ttgacaataa caacggatgg 200

gactcctgga attccatctg ggattatgga aatggctttg ctgcaaccag 250

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tgccctccat tcaatccctt gatgcactgg tcaaggaaaa gaagcttcag 350

ggtaagggac caggaggacc acctcccaag ggcctgatgt actcagtcaa 400

cccaaacaaa gtcgatgacc tgagcaagtt cggaaaaaac attgcaaaca 450

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<210> 211
<211> 185
<212> PRT
<213> Homo sapiens

<400> 211

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				20					25					30	
Asn	Asn	Ala	Gly	Ser	Gly	Gln	Gln	Ser	Val	Ser	Val	Asn	Asn	Glu	
				35					40					45	
His	Asn	Val	Ala	Asn	Val	Asp	Asn	Asn	Asn	Gly	Trp	Asp	Ser	Trp	
				50					55					60	
Asn	Ser	Ile	Trp	Asp	Tyr	Gly	Asn	Gly	Phe	Ala	Ala	Thr	Arg	Leu	
				65					70					75	
Phe	Gln	Lys	Lys	Thr	Cys	Ile	Val	His	Lys	Met	Asn	Lys	Glu	Val	
				80					85					90	
Met	Pro	Ser	Ile	Gln	Ser	Leu	Asp	Ala	Leu	Val	Lys	Glu	Lys	Lys	
				95					100					105	
Leu	Gln	Gly	Lys	Gly	Pro	Gly	Gly	Pro	Pro	Pro	Lys	Gly	Leu	Met	
				110					115					120	
Tyr	Ser	Val	Asn	Pro	Asn	Lys	Val	Asp	Asp	Leu	Ser	Lys	Phe	Gly	
				125					130					135	
Lys	Asn	Ile	Ala	Asn	Met	Cys	Arg	Gly	Ile	Pro	Thr	Tyr	Met	Ala	
				140					145					150	
Glu	Glu	Met	Gln	Glu	Ala	Ser	Leu	Phe	Phe	Tyr	Ser	Gly	Thr	Cys	
				155					160					165	
Tyr	Thr	Thr	Ser	Val	Leu	Trp	Ile	Val	Asp	Ile	Ser	Phe	Cys	Gly	
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Asp	Thr	Val	Glu	Asn											
				185											

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<212> DNA
<213> Homo sapiens

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atgaaataat ttaaaagggc ttcgctcata tataggaaaa tcgcatatgg 150

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tgtttacatg caagcttata gttgaaatat ttttcaggaa ttacatgaat 350

gacagtcttc gaaccaatgt gtttgttcga tttcaaccag agactatagc 400

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<211> 299
<212> PRT
<213> Homo sapiens

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            20                  25                  30

Gln Ile Pro Leu Pro Thr Arg Pro His Trp Phe Leu Leu Phe Gly
        35                  40                  45

Thr Thr Glu Glu Glu Ile Gln Glu Ile Cys Ile Glu Thr Leu Arg
    50                  55                  60

Leu Tyr Thr Arg Lys Lys Pro Asn Tyr Glu Leu Leu Glu Lys Glu
65                  70                  75

Val Glu Lys Arg Lys Val Ala Leu Gln Glu Ala Lys Leu Lys Ala
                80                  85                  90

Lys Gly Leu Asn Pro Asp Gly Thr Pro Ala Leu Ser Thr Leu Gly
            95                  100                 105

Gly Phe Ser Pro Ala Ser Lys Pro Ser Ser Pro Arg Glu Val Lys
        110                 115                 120

Ala Glu Glu Lys Ser Pro Ile Ser Ile Asn Val Lys Thr Val Lys
    125                 130                 135

Lys Glu Pro Glu Asp Arg Gln Gln Ala Ser Lys Ser Pro Tyr Asn
140                 145                 150

Gly Val Arg Lys Asp Ser Lys Arg Ser Arg Asn Ser Arg Ser Ala
155                 160                 165

Ser Arg Ser Arg Ser Arg Thr Arg Ser Arg Ser Arg Ser His Thr
                170                 175                 180

Pro Arg Arg His Tyr Asn Asn Arg Arg Ser Arg Ser Gly Thr Tyr
            185                 190                 195

Ser Ser Arg Ser Arg Ser Arg Ser Arg Ser His Ser Glu Ser Pro
        200                 205                 210

Arg Arg His His Asn His Gly Ser Pro His Leu Lys Ala Lys His
    215                 220                 225

Thr Arg Asp Asp Leu Lys Ser Ser Asn Arg His Gly His Lys Arg
230                 235                 240

Lys Lys Ser Arg Ser Arg Ser Gln Ser Lys Ser Arg Asp His Ser
245                 250                 255

Asp Ala Ala Lys Lys His Arg His Glu Arg Gly His His Arg Asp
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<211> 1807
<212> DNA
<213> Homo sapiens

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<210> 216

<211> 479
<212> PRT
<213> Homo sapiens

<400> 216
Met Ala Val Leu Gly Val Gln Leu Val Val Thr Leu Leu Thr Ala
1 5 10 15

Thr Leu Met His Arg Leu Ala Pro His Cys Ser Phe Ala Arg Trp
20 25 30

Leu Leu Cys Asn Gly Ser Leu Phe Arg Tyr Lys His Pro Ser Glu
35 40 45

Glu Glu Leu Arg Ala Leu Ala Gly Lys Pro Arg Pro Arg Gly Arg
50 55 60

Lys Glu Arg Trp Ala Asn Gly Leu Ser Glu Glu Lys Pro Leu Ser
65 70 75

Val Pro Arg Asp Ala Pro Phe Gln Leu Glu Thr Cys Pro Leu Thr
80 85 90

Thr Val Asp Ala Leu Val Leu Arg Phe Phe Leu Glu Tyr Gln Trp
95 100 105

Phe Val Asp Phe Ala Val Tyr Ser Gly Gly Val Tyr Leu Phe Thr
110 115 120

Glu Ala Tyr Tyr Tyr Met Leu Gly Pro Ala Lys Glu Thr Asn Ile
125 130 135

Ala Val Phe Trp Cys Leu Leu Thr Val Thr Phe Ser Ile Lys Met
140 145 150

Phe Leu Thr Val Thr Arg Leu Tyr Phe Ser Ala Glu Glu Gly Gly
155 160 165

Glu Arg Ser Val Cys Leu Thr Phe Ala Phe Leu Phe Leu Leu Leu
170 175 180

Ala Met Leu Val Gln Val Val Arg Glu Glu Thr Leu Glu Leu Gly
185 190 195

Leu Glu Pro Gly Leu Ala Ser Met Thr Gln Asn Leu Glu Pro Leu
200 205 210

Leu Lys Lys Gln Gly Trp Asp Trp Ala Leu Pro Val Ala Lys Leu
215 220 225

Ala Ile Arg Val Gly Leu Ala Val Val Gly Ser Val Leu Gly Ala
230 235 240

Phe Leu Thr Phe Pro Gly Leu Arg Leu Ala Gln Thr His Arg Asp
245 250 255

Ala Leu Thr Met Ser Glu Asp Arg Pro Met Leu Gln Phe Leu Leu
260 265 270

His Thr Ser Phe Leu Ser Pro Leu Phe Ile Leu Trp Leu Trp Thr
275 280 285

Lys Pro Ile Ala Arg Asp Phe Leu His Gln Pro Pro Phe Gly Glu

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290 295 300

Thr Arg Phe Ser Leu Leu Ser Asp Ser Ala Phe Asp Ser Gly Arg
305 310 315

Leu Trp Leu Leu Val Val Leu Cys Leu Leu Arg Leu Ala Val Thr
320 325 330

Arg Pro His Leu Gln Ala Tyr Leu Cys Leu Ala Lys Ala Arg Val
335 340 345

Glu Gln Leu Arg Arg Glu Ala Gly Arg Ile Glu Ala Arg Glu Ile
350 355 360

Gln Gln Arg Val Val Arg Val Tyr Cys Tyr Val Thr Val Val Ser
365 370 375

Leu Gln Tyr Leu Thr Pro Leu Ile Leu Thr Leu Asn Cys Thr Leu
380 385 390

Leu Leu Lys Thr Leu Gly Gly Tyr Ser Trp Gly Leu Gly Pro Ala
395 400 405

Pro Leu Leu Ser Pro Asp Pro Ser Ser Ala Ser Ala Ala Pro Ile
410 415 420

Gly Ser Gly Glu Asp Glu Val Gln Gln Thr Ala Ala Arg Ile Ala
425 430 435

Gly Ala Leu Gly Gly Leu Leu Thr Pro Leu Phe Leu Arg Gly Val
440 445 450

Leu Ala Tyr Leu Ile Trp Trp Thr Ala Ala Cys Gln Leu Leu Ala
455 460 465

Ser Leu Phe Gly Leu Tyr Phe His Gln His Leu Ala Gly Ser
470 475

<210> 217
<211> 574
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 5, 146
<223> unknown base

<400> 217
cgttngcacg cgtcaatggc ggtcctcgga gtacagctgg tggtgaccct 50

gctcactgcc accctcatgc acaggctggc gccacactgc tccttcgcgc 100

gctggctgct ctgtaacggc agtttgttcc gatacaagca cccgtnttga 150

ggaggagctt cgggccctgg cggggaagcc gaggcccaga ggcaggaaag 200

agcggtgggc caatggcctt agtgaggaga agccactgtc tgtgccccga 250

gatgccccgt tccagctgga gacctgcccc ctcacgaccg tggatgccct 300

ggtcctgcgc ttcttcctgg agtaccagtg gtttgtggac tttgctgtgt 350

actcgggcgg cgtgtacctc ttcacagagg cctactacta catgctggga 400

ccagccaagg agactaacat tgctgtgttc tggtgcctgc tcacagtgac 450

cttctccatc aagatgttcc tgacagtgac acggctgtac ttcagcgccg 500

aggaggggggg tgagcgctct gtctgcctca cctttgcctt cctcttcctg 550

ctgctggcca tgctggtgca agcg 574

<210> 218
<211> 2571
<212> DNA
<213> Homo sapiens

<400> 218
ggttcctaca tcctctcatc tgagaatcag agagcataat cttcttacgg 50

gcccgtgatt tattaacgtg gcttaatctg aaggttctca gtcaaattct 100

ttgtgatcta ctgattgtgg gggcatggca aggtttgctt aaaggagctt 150

ggctggtttg ggcccttgta gctgacagaa ggtggccagg gagaatgcag 200

cacactgctc ggagaatgaa ggcgcttctg ttgctggtct tgccttggct 250

cagtcctgct aactacattg acaatgtggg caacctgcac ttcctgtatt 300

cagaactctg taaaggtgcc tcccactacg gcctgaccaa agataggaag 350

aggcgctcac aagatggctg tccagacggc tgtgcgagcc tcacagccac 400

ggctccctcc ccagaggttt ctgcagctgc caccatctcc ttaatgacag 450

acgagcctgg cctagacaac cctgcctacg tgtcctcggc agaggacggg 500

cagccagcaa tcagcccagt ggactctggc cggagcaacc gaactagggc 550

acggcccttt gagagatcca ctattagaag cagatcattt aaaaaaataa 600

atcgagcttt gagtgttctt cgaaggacaa agagcgggag tgcagttgcc 650

aaccatgccg accagggcag ggaaaattct gaaaacacca ctgcccctga 700

agtctttcca aggttgtacc acctgattcc agatggtgaa attaccagca 750

tcaagatcaa tcgagtagat cccagtgaaa gcctctctat taggctggtg 800

ggaggtagcg aaaccccact ggtccatatc attatccaac acatttatcg 850

tgatggggtg atcgccagag acggccggct actgccagga gacatcattc 900

taaaggtcaa cgggatggac atcagcaatg tccctcacaa ctacgctgtg 950

cgtctcctgc ggcagccctg ccaggtgctg tggctgactg tgatgcgtga 1000

acagaagttc cgcagcagga acaatggaca ggccccggat gcctacagac 1050

cccgagatga cagctttcat gtgattctca acaaaagtag ccccgaggag 1100

cagcttggaa taaaactggt gcgcaaggtg gatgagcctg gggttttcat 1150

cttcaatgtg ctggatggcg gtgtggcata tcgacatggt cagcttgagg 1200

agaatgaccg tgtgttagcc atcaatggac atgatcttcg atatggcagc 1250

ccagaaagtg cggctcatct gattcaggcc agtgaaagac gtgttcacct 1300

cgtcgtgtcc cgccaggttc ggcagcggag ccctgacatc tttcaggaag 1350

ccggctggaa cagcaatggc agctggtccc cagggccagg ggagaggagc 1400

aacactccca agcccctcca tcctacaatt acttgtcatg agaaggtggt 1450

aaatatccaa aaagaccccg gtgaatctct cggcatgacc gtcgcagggg 1500

gagcatcaca tagagaatgg gatttgccta tctatgtcat cagtgttgag 1550

cccggaggag tcataagcag agatggaaga ataaaaacag gtgacatttt 1600

gttgaatgtg gatggggtcg aactgacaga ggtcagccgg agtgaggcag 1650

tggcattatt gaaaagaaca tcatcctcga tagtactcaa agctttggaa 1700

gtcaaagagt atgagcccca ggaagactgc agcagcccag cagccctgga 1750

ctccaaccac aacatggccc cacccagtga ctggtcccca tcctgggtca 1800

tgtggctgga attaccacgg tgcttgtata actgtaaaga tattgtatta 1850

cgaagaaaca cagctggaag tctgggcttc tgcattgtag gaggttatga 1900

agaatacaat ggaaacaaac ctttttttcat caaatccatt gttgaaggaa 1950

caccagcata caatgatgga agaattagat gtggtgatat tcttcttgct 2000

gtcaatggta gaagtacatc aggaatgata catgcttgct tggcaagact 2050

gctgaaagaa cttaaaggaa gaattactct aactattgtt tcttggcctg 2100

gcacttttttt atagaatcaa tgatgggtca gaggaaaaca gaaaaatcac 2150

aaataggcta agaagttgaa acactatatt tatcttgtca gtttttatat 2200

ttaaagaaag aatacattgt aaaaatgtca ggaaaagtat gatcatctaa 2250

tgaaagccag ttacacctca gaaaatatga ttccaaaaaa attaaaacta 2300

ctagtttttt ttcagtgtgg aggatttctc attactctac aacattgttt 2350

atatttttttc tattcaataa aaagccctaa aacaactaaa atgattgatt 2400

tgtatacccc actgaattca agctgattta aatttaaaat ttggtatatg 2450

ctgaagtctg ccaagggtac attatggcca tttttaattt acagctaaaa 2500

tatttttttaa aatgcattgc tgagaaacgt tgctttcatc aaacaagaat 2550

aaatattttt cagaagttaa a 2571

<210> 219
<211> 632
<212> PRT
<213> Homo sapiens

<400> 219
Met Lys Ala Leu Leu Leu Leu Val Leu Pro Trp Leu Ser Pro Ala

1 5 10 15

Asn Tyr Ile Asp Asn Val Gly Asn Leu His Phe Leu Tyr Ser Glu
20 25 30

Leu Cys Lys Gly Ala Ser His Tyr Gly Leu Thr Lys Asp Arg Lys
35 40 45

Arg Arg Ser Gln Asp Gly Cys Pro Asp Gly Cys Ala Ser Leu Thr
50 55 60

Ala Thr Ala Pro Ser Pro Glu Val Ser Ala Ala Ala Thr Ile Ser
65 70 75

Leu Met Thr Asp Glu Pro Gly Leu Asp Asn Pro Ala Tyr Val Ser
80 85 90

Ser Ala Glu Asp Gly Gln Pro Ala Ile Ser Pro Val Asp Ser Gly
95 100 105

Arg Ser Asn Arg Thr Arg Ala Arg Pro Phe Glu Arg Ser Thr Ile
110 115 120

Arg Ser Arg Ser Phe Lys Lys Ile Asn Arg Ala Leu Ser Val Leu
125 130 135

Arg Arg Thr Lys Ser Gly Ser Ala Val Ala Asn His Ala Asp Gln
140 145 150

Gly Arg Glu Asn Ser Glu Asn Thr Thr Ala Pro Glu Val Phe Pro
155 160 165

Arg Leu Tyr His Leu Ile Pro Asp Gly Glu Ile Thr Ser Ile Lys
170 175 180

Ile Asn Arg Val Asp Pro Ser Glu Ser Leu Ser Ile Arg Leu Val
185 190 195

Gly Gly Ser Glu Thr Pro Leu Val His Ile Ile Ile Gln His Ile
200 205 210

Tyr Arg Asp Gly Val Ile Ala Arg Asp Gly Arg Leu Leu Pro Gly
215 220 225

Asp Ile Ile Leu Lys Val Asn Gly Met Asp Ile Ser Asn Val Pro
230 235 240

His Asn Tyr Ala Val Arg Leu Leu Arg Gln Pro Cys Gln Val Leu
245 250 255

Trp Leu Thr Val Met Arg Glu Gln Lys Phe Arg Ser Arg Asn Asn
260 265 270

Gly Gln Ala Pro Asp Ala Tyr Arg Pro Arg Asp Asp Ser Phe His
275 280 285

Val Ile Leu Asn Lys Ser Ser Pro Glu Glu Gln Leu Gly Ile Lys
290 295 300

Leu Val Arg Lys Val Asp Glu Pro Gly Val Phe Ile Phe Asn Val
305 310 315

Leu Asp Gly Gly Val Ala Tyr Arg His Gly Gln Leu Glu Glu Asn

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320 325 330

Asp Arg Val Leu Ala Ile Asn Gly His Asp Leu Arg Tyr Gly Ser
335 340 345

Pro Glu Ser Ala Ala His Leu Ile Gln Ala Ser Glu Arg Arg Val
350 355 360

His Leu Val Val Ser Arg Gln Val Arg Gln Arg Ser Pro Asp Ile
365 370 375

Phe Gln Glu Ala Gly Trp Asn Ser Asn Gly Ser Trp Ser Pro Gly
380 385 390

Pro Gly Glu Arg Ser Asn Thr Pro Lys Pro Leu His Pro Thr Ile
395 400 405

Thr Cys His Glu Lys Val Val Asn Ile Gln Lys Asp Pro Gly Glu
410 415 420

Ser Leu Gly Met Thr Val Ala Gly Gly Ala Ser His Arg Glu Trp
425 430 435

Asp Leu Pro Ile Tyr Val Ile Ser Val Glu Pro Gly Gly Val Ile
440 445 450

Ser Arg Asp Gly Arg Ile Lys Thr Gly Asp Ile Leu Leu Asn Val
455 460 465

Asp Gly Val Glu Leu Thr Glu Val Ser Arg Ser Glu Ala Val Ala
470 475 480

Leu Leu Lys Arg Thr Ser Ser Ser Ile Val Leu Lys Ala Leu Glu
485 490 495

Val Lys Glu Tyr Glu Pro Gln Glu Asp Cys Ser Ser Pro Ala Ala
500 505 510

Leu Asp Ser Asn His Asn Met Ala Pro Pro Ser Asp Trp Ser Pro
515 520 525

Ser Trp Val Met Trp Leu Glu Leu Pro Arg Cys Leu Tyr Asn Cys
530 535 540

Lys Asp Ile Val Leu Arg Arg Asn Thr Ala Gly Ser Leu Gly Phe
545 550 555

Cys Ile Val Gly Gly Tyr Glu Glu Tyr Asn Gly Asn Lys Pro Phe
560 565 570

Phe Ile Lys Ser Ile Val Glu Gly Thr Pro Ala Tyr Asn Asp Gly
575 580 585

Arg Ile Arg Cys Gly Asp Ile Leu Leu Ala Val Asn Gly Arg Ser
590 595 600

Thr Ser Gly Met Ile His Ala Cys Leu Ala Arg Leu Leu Lys Glu
605 610 615

Leu Lys Gly Arg Ile Thr Leu Thr Ile Val Ser Trp Pro Gly Thr
620 625 630

Phe Leu

<210> 220
<211> 773
<212> DNA
<213> Homo sapiens

<400> 220
ccaaagtgat catttgaaaa agagatatcc acatcttcaa gcccatataa 50

aggatagaag ctgcacaggg cagctttact tactccagca ccttcctctc 100

ccaggcaaat ggtgctgacc atctttggga tacaatctca tggatacgag 150

gtttttaaca tcatcagccc aagcaacaat ggtggcaatg ttcaggagac 200

agtgacaatt gataatgaaa aaaataccgc catcgttaac atccatgcag 250

gatcatgctc ttctaccaca atttttgact ataaacatgg ctacattgca 300

tccagggtgc tctcccgaag agcctgcttt atcctgaaga tggaccatca 350

gaacatccct cctctgaaca atctccaatg gtacatctat gagaaacagg 400

ctctggacaa catgttctcc aacaaataca cctgggtcaa gtacaaccct 450

ctggagtctc tgatcaaaga cgtggattgg ttcctgcttg ggtcacccat 500

tgagaaactc tgcaaacata tccctttgta taaggggaa gtggttgaaa 550

acacacataa tgtcggtgct ggaggctgtg caaaggctgg gctcctgggc 600

atcttgggaa tttcaatctg tgcagacatt catgtttagg atgattagcc 650

ctcttgtttt atcttttcaa agaaatacat ccttggttta cactcaaaag 700

tcaaattaaa ttctttccca atgccccaac taattttgag attcagtcag 750

aaaatataaa tgctgtattt ata 773

<210> 221
<211> 184
<212> PRT
<213> Homo sapiens

<400> 221
Met Lys Ile Leu Val Ala Phe Leu Val Val Leu Thr Ile Phe Gly
1 5 10 15

Ile Gln Ser His Gly Tyr Glu Val Phe Asn Ile Ile Ser Pro Ser
20 25 30

Asn Asn Gly Gly Asn Val Gln Glu Thr Val Thr Ile Asp Asn Glu
35 40 45

Lys Asn Thr Ala Ile Val Asn Ile His Ala Gly Ser Cys Ser Ser
50 55 60

Thr Thr Ile Phe Asp Tyr Lys His Gly Tyr Ile Ala Ser Arg Val
65 70 75

Leu Ser Arg Arg Ala Cys Phe Ile Leu Lys Met Asp His Gln Asn
80 85 90

Ile Pro Pro Leu Asn Asn Leu Gln Trp Tyr Ile Tyr Glu Lys Gln
95 100 105

Ala Leu Asp Asn Met Phe Ser Asn Lys Tyr Thr Trp Val Lys Tyr
110 115 120

Asn Pro Leu Glu Ser Leu Ile Lys Asp Val Asp Trp Phe Leu Leu
125 130 135

Gly Ser Pro Ile Glu Lys Leu Cys Lys His Ile Pro Leu Tyr Lys
140 145 150

Gly Glu Val Val Glu Asn Thr His Asn Val Gly Ala Gly Gly Cys
155 160 165

Ala Lys Ala Gly Leu Leu Gly Ile Leu Gly Ile Ser Ile Cys Ala
170 175 180

Asp Ile His Val

<210> 222
<211> 992
<212> DNA
<213> Homo sapiens

<400> 222
ggcacgagcc aggaactagg aggttctcac tgcccgagca gaggccctac 50

acccaccgag gcatggggct ccctgggctg ttctgcttgg ccgtgctggc 100

tgccagcagc ttctccaagg cacgggagga agaaattacc cctgtggtct 150

ccattgccta caaagtcctg gaagttttcc ccaaaggccg ctgggtgctc 200

ataacctgct gtgcacccca gccaccaccg cccatcacct attccctctg 250

tggaaccaag aacatcaagg tggccaagaa ggtggtgaag acccacgagc 300

cggcctcctt caacctcaac gtcacactca agtccagtcc agacctgctc 350

acctacttct gccgggcgtc ctccacctca ggtgcccatg tggacagtgc 400

caggctacag atgcactggg agctgtggtc caagccagtg tctgagctgc 450

gggccaactt cactctgcag gacagagggg caggccccag ggtggagatg 500

atctgccagg cgtcctcggg cagcccacct atcaccaaca gcctgatcgg 550

gaaggatggg caggtccacc tgcagcagag accatgccac aggcagcctg 600

ccaacttctc cttcctgccg agccagacat cggactggtt ctggtgccag 650

gctgcaaaca acgccaatgt ccagcacagc gccctcacag tggtgccccc 700

aggtggtgac cagaagatgg aggactggca gggtcccctg gagagcccca 750

tccttgcctt gccgctctac aggagcaccc gccgtctgag tgaagaggag 800

tttgggggggt tcaggatagg gaatggggag gtcagaggac gcaaagcagc 850

agccatgtag aatgaaccgt ccagagagcc aagcacggca gaggactgca 900

ggccatcagc gtgcactgtt cgtatttgga gttcatgcaa aatgagtgtg 950

ttttagctgc tcttgccaca aaaaaaaaaa aaaaaaaaaa aa 992

<210> 223
<211> 265
<212> PRT
<213> Homo sapiens

<400> 223

Met Gly Leu Pro Gly Leu Phe Cys Leu Ala Val Leu Ala Ala Ser
1 5 10 15

Ser Phe Ser Lys Ala Arg Glu Glu Glu Ile Thr Pro Val Val Ser
20 25 30

Ile Ala Tyr Lys Val Leu Glu Val Phe Pro Lys Gly Arg Trp Val
35 40 45

Leu Ile Thr Cys Cys Ala Pro Gln Pro Pro Pro Pro Ile Thr Tyr
50 55 60

Ser Leu Cys Gly Thr Lys Asn Ile Lys Val Ala Lys Lys Val Val
65 70 75

Lys Thr His Glu Pro Ala Ser Phe Asn Leu Asn Val Thr Leu Lys
80 85 90

Ser Ser Pro Asp Leu Leu Thr Tyr Phe Cys Arg Ala Ser Ser Thr
95 100 105

Ser Gly Ala His Val Asp Ser Ala Arg Leu Gln Met His Trp Glu
110 115 120

Leu Trp Ser Lys Pro Val Ser Glu Leu Arg Ala Asn Phe Thr Leu
125 130 135

Gln Asp Arg Gly Ala Gly Pro Arg Val Glu Met Ile Cys Gln Ala
140 145 150

Ser Ser Gly Ser Pro Pro Ile Thr Asn Ser Leu Ile Gly Lys Asp
155 160 165

Gly Gln Val His Leu Gln Gln Arg Pro Cys His Arg Gln Pro Ala
170 175 180

Asn Phe Ser Phe Leu Pro Ser Gln Thr Ser Asp Trp Phe Trp Cys
185 190 195

Gln Ala Ala Asn Asn Ala Asn Val Gln His Ser Ala Leu Thr Val
200 205 210

Val Pro Pro Gly Gly Asp Gln Lys Met Glu Asp Trp Gln Gly Pro
215 220 225

Leu Glu Ser Pro Ile Leu Ala Leu Pro Leu Tyr Arg Ser Thr Arg
230 235 240

Arg Leu Ser Glu Glu Glu Phe Gly Gly Phe Arg Ile Gly Asn Gly
245 250 255

Glu Val Arg Gly Arg Lys Ala Ala Ala Met
260 265

<210> 224
<211> 1297
<212> DNA
<213> Homo sapiens

<400> 224
ggtccttaat ggcagcagcc gccgctacca agatccttct gtgcctcccg 50

cttctgctcc tgctgtccgg ctggtcccgg gctgggcgag ccgaccctca 100

ctctctttgc tatgacatca ccgtcatccc taagttcaga cctggaccac 150

ggtggtgtgc ggttcaaggc caggtggatg aaaagacttt tcttcactat 200

gactgtggca acaagacagt cacacctgtc agtcccctgg ggaagaaact 250

aaatgtcaca acggcctgga aagcacagaa cccagtactg agagaggtgg 300

tggacatact tacagagcaa ctgcgtgaca ttcagctgga gaattacaca 350

cccaaggaac ccctcaccct gcaggcaagg atgtcttgtg agcagaaagc 400

tgaaggacac agcagtggat cttggcagtt cagtttcgat gggcagatct 450

tcctcctctt tgactcagag aagagaatgt ggacaacggt tcatcctgga 500

gccagaaaga tgaaagaaaa gtgggagaat gacaaggttg tggccatgtc 550

cttccattac ttctcaatgg gagactgtat aggatggctt gaggacttct 600

tgatgggcat ggacagcacc ctggagccaa gtgcaggagc accactcgcc 650

atgtcctcag gcacaaccca actcagggcc acagccacca ccctcatcct 700

ttgctgcctc ctcatcatcc tcccctgctt catcctccct ggcatctgag 750

gagagtcctt tagagtgaca ggttaaagct gataccaaaa ggctcctgtg 800

agcacggtct tgatcaaact cgcccttctg tctggccagc tgcccacgac 850

ctacggtgta tgtccagtgg cctccagcag atcatgatga catcatggac 900

ccaatagctc attcactgcc ttgattcctt ttgccaacaa ttttaccagc 950

agttatacct aacatattat gcaatttttct cttggtgcta cctgatggaa 1000

ttcctgcact taaagttctg gctgactaaa caagatatat cattttcttt 1050

cttctctttt tgtttggaaa atcaagtact tctttgaatg atgatctctt 1100

tcttgcaaat gatattgtca gtaaaataat cacgttagac ttcagacctc 1150

tggggattct ttccgtgtcc tgaaagagaa tttttaaatt atttaataag 1200

aaaaaattta tattaatgat tgtttccttt agtaatttat tgttctgtac 1250

tgatatttaa ataaagagtt ctatttccca aaaaaaaaaa aaaaaaa 1297

<210> 225
<211> 246
<212> PRT
<213> Homo sapiens

<400> 225
Met Ala Ala Ala Ala Ala Thr Lys Ile Leu Leu Cys Leu Pro Leu
1 5 10 15

Leu Leu Leu Leu Ser Gly Trp Ser Arg Ala Gly Arg Ala Asp Pro
20 25 30

His Ser Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg Pro
35 40 45

Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr
50 55 60

Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser
65 70 75

Pro Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln
80 85 90

Asn Pro Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu
95 100 105

Arg Asp Ile Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr
110 115 120

Leu Gln Ala Arg Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser
125 130 135

Ser Gly Ser Trp Gln Phe Ser Phe Asp Gly Gln Ile Phe Leu Leu
140 145 150

Phe Asp Ser Glu Lys Arg Met Trp Thr Thr Val His Pro Gly Ala
155 160 165

Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys Val Val Ala Met
170 175 180

Ser Phe His Tyr Phe Ser Met Gly Asp Cys Ile Gly Trp Leu Glu
185 190 195

Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser Ala Gly
200 205 210

Ala Pro Leu Ala Met Ser Ser Gly Thr Thr Gln Leu Arg Ala Thr
215 220 225

Ala Thr Thr Leu Ile Leu Cys Cys Leu Leu Ile Ile Leu Pro Cys
230 235 240

Phe Ile Leu Pro Gly Ile
245

<210> 226
<211> 735
<212> DNA
<213> Homo sapiens

<400> 226
gggaaagcca tttcgaaaac ccatctatac aaactatata ttttcatttc 50

tgctgctagc tgccttgggc ctcacaattt tcattctgtt ttctgacttt 100

caagttatat accgtggaat ggagttgatc ccaaccataa catcgtggag 150

ggttttaatt ttggtggtag ccctcaccca attctggtgt ggctttcttt 200

gcagaggatt ccaccttcaa aatcatgaac tctggctgtt gatcaaaaga 250

gaatttggat tctactctaa aagtcaatat aggacttggc aaaagaagct 300

agcagaagac tcaacctggc ctcccataaa caggacagat tattcaggtg 350

atggcaaaaa tggattctac atcaacggag gctatgaaag ccatgaacag 400

attccaaaaa gaaaactcaa attgggaggc caacccacag aacagcattt 450

ctgggccagg ctgtaatcag aattgtcgtc gtacatgctc aacagcattg 500

ctttttcccc caaaattaac acattgtgga gaagtgatga tactctcccc 550

ttacctttcc tctctccatt caagcattca aagtatattt tcaatgaatt 600

aaaccttgca gcaagggacc ttagataggc ttattctgac tgtatgcttt 650

accaatgaga gaaaaaaatg catttcctgt atcatccttt tcaataaact 700

gtattcattt tgaaaaaaaa aaaaaaaaaa aaaaa 735

<210> 227
<211> 115
<212> PRT
<213> Homo sapiens

<400> 227

Met	Glu	Leu	Ile	Pro	Thr	Ile	Thr	Ser	Trp	Arg	Val	Leu	Ile	Leu	
1				5				10						15	
Val	Val	Ala	Leu	Thr	Gln	Phe	Trp	Cys	Gly	Phe	Leu	Cys	Arg	Gly	
				20				25						30	
Phe	His	Leu	Gln	Asn	His	Glu	Leu	Trp	Leu	Leu	Ile	Lys	Arg	Glu	
				35				40						45	
Phe	Gly	Phe	Tyr	Ser	Lys	Ser	Gln	Tyr	Arg	Thr	Trp	Gln	Lys	Lys	
				50				55						60	
Leu	Ala	Glu	Asp	Ser	Thr	Trp	Pro	Pro	Ile	Asn	Arg	Thr	Asp	Tyr	
				65				70						75	
Ser	Gly	Asp	Gly	Lys	Asn	Gly	Phe	Tyr	Ile	Asn	Gly	Gly	Tyr	Glu	
				80				85						90	
Ser	His	Glu	Gln	Ile	Pro	Lys	Arg	Lys	Leu	Lys	Leu	Gly	Gly	Gln	
				95				100						105	
Pro	Thr	Glu	Gln	His	Phe	Trp	Ala	Arg	Leu						
				110				115							

<210> 228
<211> 2185
<212> DNA
<213> Homo sapiens

<400> 228
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cacaccatga agctcttgtg gcaggtaact gtgcaccacc acacctggaa 100

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gtgcagccat cgctgctgcc gcctcagccg ggccccagaa ctgcccctcc 200

gtttgctcgt gcagtaacca gttcagcaag gtggtgtgca cgcgccgggg 250

cctctccgag gtcccgcagg gtattccctc gaacacccgg tacctcaacc 300

tcatggagaa caacatccag atgatccagg ccgacacctt ccgccacctc 350

caccacctgg aggtcctgca gttgggcagg aactccatcc ggcagattga 400

ggtgggggcc ttcaacggcc tggccagcct caacaccctg gagctgttcg 450

acaactggct gacagtcatc cctagcgggg cctttgaata cctgtccaag 500

ctgcgggagc tctggcttcg caacaacccc atcgaaagca tcccctctta 550

cgccttcaac cgggtgccct ccctcatgcg cctggacttg ggggagctca 600

agaagctgga gtatatctct gagggagctt ttgaggggct gttcaacctc 650

aagtatctga acttgggcat gtgcaacatt aaagacatgc ccaatctcac 700

ccccctggtg gggctggagg agctggagat gtcagggaac cacttccctg 750

agatcaggcc tggctccttc catggcctga gctccctcaa gaagctctgg 800

gtcatgaact cacaggtcag cctgattgag cggaatgctt ttgacgggct 850

ggcttcactt gtggaactca acttggccca caataacctc tcttctttgc 900

cccatgacct ctttaccccg ctgaggtacc tggtggagtt gcatctacac 950

cacaaccctt ggaactgtga ttgtgacatt ctgtggctag cctggtggct 1000

tcgagagtat atacccacca attccacctg ctgtggccgc tgtcatgctc 1050

ccatgcacat gcgaggccgc tacctcgtgg aggtggacca ggcctccttc 1100

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gttaccagcc ggcatatacc acctctacca cggtgctcat tcagactacc 1550

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cccacaattc atgaccatat taactacaac acctacaaac cagcacatgg 1900

ggcccactgg acagaaaaca gcctggggaa ctctctgcac cccacagtca 1950

ccactatctc tgaaccttat ataattcaga cccataccaa ggacaaggta 2000

caggaaactc aaatatgact cccctccccc aaaaaactta taaaatgcaa 2050

tagaatgcac acaaagacag caacttttgt acagagtggg gagagacttt 2100

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attatattaa aatttaaaga caaaaagtca aaaca 2185

<210> 229
<211> 653
<212> PRT
<213> Homo sapiens

<400> 229

Met	Lys	Leu	Leu	Trp	Gln	Val	Thr	Val	His	His	His	Thr	Trp	Asn		
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Ala	Ile	Leu	Leu	Pro	Phe	Val	Tyr	Leu	Thr	Ala	Gln	Val	Trp	Ile		
				20					25						30	
Leu	Cys	Ala	Ala	Ile	Ala	Ala	Ala	Ala	Ser	Ala	Gly	Pro	Gln	Asn		
				35					40						45	
Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val	Val		
				50					55						60	
Cys	Thr	Arg	Arg	Gly	Leu	Ser	Glu	Val	Pro	Gln	Gly	Ile	Pro	Ser		
				65					70						75	
Asn	Thr	Arg	Tyr	Leu	Asn	Leu	Met	Glu	Asn	Asn	Ile	Gln	Met	Ile		
				80					85						90	
Gln	Ala	Asp	Thr	Phe	Arg	His	Leu	His	His	Leu	Glu	Val	Leu	Gln		
				95					100						105	
Leu	Gly	Arg	Asn	Ser	Ile	Arg	Gln	Ile	Glu	Val	Gly	Ala	Phe	Asn		
				110					115						120	
Gly	Leu	Ala	Ser	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Trp	Leu		
				125					130						135	
Thr	Val	Ile	Pro	Ser	Gly	Ala	Phe	Glu	Tyr	Leu	Ser	Lys	Leu	Arg		
				140					145						150	
Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser	Tyr		
				155					160						165	
Ala	Phe	Asn	Arg	Val	Pro	Ser	Leu	Met	Arg	Leu	Asp	Leu	Gly	Glu		
				170					175						180	
Leu	Lys	Lys	Leu	Glu	Tyr	Ile	Ser	Glu	Gly	Ala	Phe	Glu	Gly	Leu		

185 190 195

Phe Asn Leu Lys Tyr Leu Asn Leu Gly Met Cys Asn Ile Lys Asp
200 205 210

Met Pro Asn Leu Thr Pro Leu Val Gly Leu Glu Glu Leu Glu Met
215 220 225

Ser Gly Asn His Phe Pro Glu Ile Arg Pro Gly Ser Phe His Gly
230 235 240

Leu Ser Ser Leu Lys Lys Leu Trp Val Met Asn Ser Gln Val Ser
245 250 255

Leu Ile Glu Arg Asn Ala Phe Asp Gly Leu Ala Ser Leu Val Glu
260 265 270

Leu Asn Leu Ala His Asn Asn Leu Ser Ser Leu Pro His Asp Leu
275 280 285

Phe Thr Pro Leu Arg Tyr Leu Val Glu Leu His Leu His His Asn
290 295 300

Pro Trp Asn Cys Asp Cys Asp Ile Leu Trp Leu Ala Trp Trp Leu
305 310 315

Arg Glu Tyr Ile Pro Thr Asn Ser Thr Cys Cys Gly Arg Cys His
320 325 330

Ala Pro Met His Met Arg Gly Arg Tyr Leu Val Glu Val Asp Gln
335 340 345

Ala Ser Phe Gln Cys Ser Ala Pro Phe Ile Met Asp Ala Pro Arg
350 355 360

Asp Leu Asn Ile Ser Glu Gly Arg Met Ala Glu Leu Lys Cys Arg
365 370 375

Thr Pro Pro Met Ser Ser Val Lys Trp Leu Leu Pro Asn Gly Thr
380 385 390

Val Leu Ser His Ala Ser Arg His Pro Arg Ile Ser Val Leu Asn
395 400 405

Asp Gly Thr Leu Asn Phe Ser His Val Leu Leu Ser Asp Thr Gly
410 415 420

Val Tyr Thr Cys Met Val Thr Asn Val Ala Gly Asn Ser Asn Ala
425 430 435

Ser Ala Tyr Leu Asn Val Ser Thr Ala Glu Leu Asn Thr Ser Asn
440 445 450

Tyr Ser Phe Phe Thr Thr Val Thr Val Glu Thr Thr Glu Ile Ser
455 460 465

Pro Glu Asp Thr Thr Arg Lys Tyr Lys Pro Val Pro Thr Thr Ser
470 475 480

Thr Gly Tyr Gln Pro Ala Tyr Thr Thr Ser Thr Thr Val Leu Ile
485 490 495

Gln Thr Thr Arg Val Pro Lys Gln Val Ala Val Pro Ala Thr Asp

500 505 510

Thr Thr Asp Lys Met Gln Thr Ser Leu Asp Glu Val Met Lys Thr
515 520 525

Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Val Thr Leu Leu Ala
530 535 540

Ala Ala Met Leu Ile Val Phe Tyr Lys Leu Arg Lys Arg His Gln
545 550 555

Gln Arg Ser Thr Val Thr Ala Ala Arg Thr Val Glu Ile Ile Gln
560 565 570

Val Asp Glu Asp Ile Pro Ala Ala Thr Ser Ala Ala Ala Thr Ala
575 580 585

Ala Pro Ser Gly Val Ser Gly Glu Gly Ala Val Val Leu Pro Thr
590 595 600

Ile His Asp His Ile Asn Tyr Asn Thr Tyr Lys Pro Ala His Gly
605 610 615

Ala His Trp Thr Glu Asn Ser Leu Gly Asn Ser Leu His Pro Thr
620 625 630

Val Thr Thr Ile Ser Glu Pro Tyr Ile Ile Gln Thr His Thr Lys
635 640 645

Asp Lys Val Gln Glu Thr Gln Ile
650

<210> 230
<211> 2846
<212> DNA
<213> Homo sapiens

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tggggctcac ttttcttcag ctccttctca tctcgtcctt gccaagagag 100

tacacagtca ttaatgaagc ctgccctgga gcagagtgga atatcatgtg 150

tcgggagtgc tgtgaatatg atcagattga gtgcgtctgc cccggaaaga 200

gggaagtcgt gggttatacc atcccttgct gcaggaatga ggagaatgag 250

tgtgactcct gcctgatcca cccaggttgt accatctttg aaaactgcaa 300

gagctgccga aatggctcat gggggggtac cttggatgac ttctatgtga 350

aggggttcta ctgtgcagag tgccgagcag gctggtacgg aggagactgc 400

atgcgatgtg gccaggttct gcgagcccca aagggtcaga ttttgttgga 450

aagctatccc ctaaatgctc actgtgaatg gaccattcat gctaaacctg 500

ggtttgtcat ccaactaaga tttgtcatgt tgagtctgga gtttgactac 550

atgtgccagt atgactatgt tgaggttcgt gatggagaca accgcgatgg 600

ccagatcatc aagcgtgtct gtggcaacga gcggccagct cctatccaga 650

gcataggatc ctcactccac gtcctcttcc actccgatgg ctccaagaat 700

tttgacggtt tccatgccat ttatgaggag atcacagcat gctcctcatc 750

cccttgtttc catgacggca cgtgcgtcct tgacaaggct ggatcttaca 800

agtgtgcctg cttggcaggc tatactgggc agcgctgtga aaatctcctt 850

gaagaaagaa actgctcaga ccctgggggc ccagtcaatg ggtaccagaa 900

aataacaggg ggccctgggc ttatcaacgg acgccatgct aaaattggca 950

ccgtggtgtc tttcttttgt aacaactcct atgttcttag tggcaatgag 1000

aaaagaactt gccagcagaa tggagagtgg tcagggaaac agcccatctg 1050

cataaaagcc tgccgagaac caaagatttc agacctggtg agaaggagag 1100

ttcttccgat gcaggttcag tcaagggaga caccattaca ccagctatac 1150

tcagcggcct tcagcaagca gaaactgcag agtgccccta ccaagaagcc 1200

agcccttccc tttggagatc tgcccatggg ataccaacat ctgcataccc 1250

agctccagta tgagtgcatc tcacccttct accgccgcct gggcagcagc 1300

aggaggacat gtctgaggac tgggaagtgg agtgggcggg caccatcctg 1350

catccctatc tgcgggaaaa ttgagaacat cactgctcca aagacccaag 1400

ggttgcgctg gccgtggcag gcagccatct acaggaggac cagcggggtg 1450

catgacggca gcctacacaa gggagcgtgg ttcctagtct gcagcggtgc 1500

cctggtgaat gagcgcactg tggtggtggc tgcccactgt gttactgacc 1550

tggggaaggt caccatgatc aagacagcag acctgaaagt tgttttgggg 1600

aaattctacc gggatgatga ccgggatgag aagaccatcc agagcctaca 1650

gatttctgct atcattctgc atcccaacta tgaccccatc ctgcttgatg 1700

ctgacatcgc catcctgaag ctcctagaca aggcccgtat cagcacccga 1750

gtccagccca tctgcctcgc tgccagtcgg gatctcagca cttccttcca 1800

ggagtcccac atcactgtgg ctggctggaa tgtcctggca gacgtgagga 1850

gccctggctt caagaacgac acactgcgct ctggggtggt cagtgtggtg 1900

gactcgctgc tgtgtgagga gcagcatgag gaccatggca tcccagtgag 1950

tgtcactgat aacatgttct gtgccagctg ggaacccact gccccttctg 2000

atatctgcac tgcagagaca ggaggcatcg cggctgtgtc cttcccggga 2050

cgagcatctc ctgagccacg ctggcatctg atgggactgg tcagctggag 2100

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tgccttttaa agactggatt gaaagaaata tgaaatgaac catgctcatg 2200

cactccttga gaagtgtttc tgtatatccg tctgtacgtg tgtcattgcg 2250

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aacctctcca ctccactgac ctggtggtct tccccaactt tcagttatac 2500

gaatgccatc agcttgacca gggaagatct gggcttcatg aggccccttt 2550

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gcttctgaac tacaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2750

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2800

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2846

<210> 231
<211> 720
<212> PRT
<213> Homo sapiens

<400> 231

Met	Glu	Leu	Gly	Cys	Trp	Thr	Gln	Leu	Gly	Leu	Thr	Phe	Leu	Gln	
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Leu	Leu	Leu	Ile	Ser	Ser	Leu	Pro	Arg	Glu	Tyr	Thr	Val	Ile	Asn	
			20					25						30	
Glu	Ala	Cys	Pro	Gly	Ala	Glu	Trp	Asn	Ile	Met	Cys	Arg	Glu	Cys	
			35					40						45	
Cys	Glu	Tyr	Asp	Gln	Ile	Glu	Cys	Val	Cys	Pro	Gly	Lys	Arg	Glu	
			50					55						60	
Val	Val	Gly	Tyr	Thr	Ile	Pro	Cys	Cys	Arg	Asn	Glu	Glu	Asn	Glu	
			65					70						75	
Cys	Asp	Ser	Cys	Leu	Ile	His	Pro	Gly	Cys	Thr	Ile	Phe	Glu	Asn	
			80					85						90	
Cys	Lys	Ser	Cys	Arg	Asn	Gly	Ser	Trp	Gly	Gly	Thr	Leu	Asp	Asp	
			95					100						105	
Phe	Tyr	Val	Lys	Gly	Phe	Tyr	Cys	Ala	Glu	Cys	Arg	Ala	Gly	Trp	
			110					115						120	
Tyr	Gly	Gly	Asp	Cys	Met	Arg	Cys	Gly	Gln	Val	Leu	Arg	Ala	Pro	
			125					130						135	
Lys	Gly	Gln	Ile	Leu	Leu	Glu	Ser	Tyr	Pro	Leu	Asn	Ala	His	Cys	
			140					145						150	
Glu	Trp	Thr	Ile	His	Ala	Lys	Pro	Gly	Phe	Val	Ile	Gln	Leu	Arg	
			155					160						165	

Phe Val Met Leu Ser Leu Glu Phe Asp Tyr Met Cys Gln Tyr Asp
170 175 180

Tyr Val Glu Val Arg Asp Gly Asp Asn Arg Asp Gly Gln Ile Ile
185 190 195

Lys Arg Val Cys Gly Asn Glu Arg Pro Ala Pro Ile Gln Ser Ile
200 205 210

Gly Ser Ser Leu His Val Leu Phe His Ser Asp Gly Ser Lys Asn
215 220 225

Phe Asp Gly Phe His Ala Ile Tyr Glu Glu Ile Thr Ala Cys Ser
230 235 240

Ser Ser Pro Cys Phe His Asp Gly Thr Cys Val Leu Asp Lys Ala
245 250 255

Gly Ser Tyr Lys Cys Ala Cys Leu Ala Gly Tyr Thr Gly Gln Arg
260 265 270

Cys Glu Asn Leu Leu Glu Glu Arg Asn Cys Ser Asp Pro Gly Gly
275 280 285

Pro Val Asn Gly Tyr Gln Lys Ile Thr Gly Gly Pro Gly Leu Ile
290 295 300

Asn Gly Arg His Ala Lys Ile Gly Thr Val Val Ser Phe Phe Cys
305 310 315

Asn Asn Ser Tyr Val Leu Ser Gly Asn Glu Lys Arg Thr Cys Gln
320 325 330

Gln Asn Gly Glu Trp Ser Gly Lys Gln Pro Ile Cys Ile Lys Ala
335 340 345

Cys Arg Glu Pro Lys Ile Ser Asp Leu Val Arg Arg Arg Val Leu
350 355 360

Pro Met Gln Val Gln Ser Arg Glu Thr Pro Leu His Gln Leu Tyr
365 370 375

Ser Ala Ala Phe Ser Lys Gln Lys Leu Gln Ser Ala Pro Thr Lys
380 385 390

Lys Pro Ala Leu Pro Phe Gly Asp Leu Pro Met Gly Tyr Gln His
395 400 405

Leu His Thr Gln Leu Gln Tyr Glu Cys Ile Ser Pro Phe Tyr Arg
410 415 420

Arg Leu Gly Ser Ser Arg Arg Thr Cys Leu Arg Thr Gly Lys Trp
425 430 435

Ser Gly Arg Ala Pro Ser Cys Ile Pro Ile Cys Gly Lys Ile Glu
440 445 450

Asn Ile Thr Ala Pro Lys Thr Gln Gly Leu Arg Trp Pro Trp Gln
455 460 465

Ala Ala Ile Tyr Arg Arg Thr Ser Gly Val His Asp Gly Ser Leu
470 475 480

His Lys Gly Ala Trp Phe Leu Val Cys Ser Gly Ala Leu Val Asn
485 490 495

Glu Arg Thr Val Val Val Ala Ala His Cys Val Thr Asp Leu Gly
500 505 510

Lys Val Thr Met Ile Lys Thr Ala Asp Leu Lys Val Val Leu Gly
515 520 525

Lys Phe Tyr Arg Asp Asp Asp Arg Asp Glu Lys Thr Ile Gln Ser
530 535 540

Leu Gln Ile Ser Ala Ile Ile Leu His Pro Asn Tyr Asp Pro Ile
545 550 555

Leu Leu Asp Ala Asp Ile Ala Ile Leu Lys Leu Leu Asp Lys Ala
560 565 570

Arg Ile Ser Thr Arg Val Gln Pro Ile Cys Leu Ala Ala Ser Arg
575 580 585

Asp Leu Ser Thr Ser Phe Gln Glu Ser His Ile Thr Val Ala Gly
590 595 600

Trp Asn Val Leu Ala Asp Val Arg Ser Pro Gly Phe Lys Asn Asp
605 610 615

Thr Leu Arg Ser Gly Val Val Ser Val Val Asp Ser Leu Leu Cys
620 625 630

Glu Glu Gln His Glu Asp His Gly Ile Pro Val Ser Val Thr Asp
635 640 645

Asn Met Phe Cys Ala Ser Trp Glu Pro Thr Ala Pro Ser Asp Ile
650 655 660

Cys Thr Ala Glu Thr Gly Gly Ile Ala Ala Val Ser Phe Pro Gly
665 670 675

Arg Ala Ser Pro Glu Pro Arg Trp His Leu Met Gly Leu Val Ser
680 685 690

Trp Ser Tyr Asp Lys Thr Cys Ser His Arg Leu Ser Thr Ala Phe
695 700 705

Thr Lys Val Leu Pro Phe Lys Asp Trp Ile Glu Arg Asn Met Lys
710 715 720

<210> 232
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 232
aggttcgtga tggagacaac cgcg 24

<210> 233
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 233
tgtcaaggac gcactgccgt catg 24

<210> 234
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 234
tggccagatc atcaagcgtg tctgtggcaa cgagcggcca gctcctatcc 50

<210> 235
<211> 1964
<212> DNA
<213> Homo sapiens

<400> 235
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agctcaactt gaagctttct tgcctgcagt gaagcagaga gatagatatt 100

attcacgtaa taaaaaacat gggcttcaac ctgactttcc acctttccta 150

caaattccga ttactgttgc tgttgacttt gtgcctgaca gtggttgggt 200

gggccaccag taactacttc gtgggtgcca ttcaagagat tcctaaagca 250

aaggagttca tggctaattt ccataagacc ctcattttgg ggaagggaaa 300

aactctgact aatgaagcat ccacgaagaa ggtagaactt gacaactgtc 350

cttctgtgtc tccttacctc agaggccaga gcaagctcat tttcaaacca 400

gatctcactt tggaagaggt acaggcagaa aatcccaaag tgtccagagg 450

ccggtatcgc cctcaggaat gtaaagcttt acagagggtc gccatcctcg 500

ttccccaccg gaacagagag aaacacctga tgtacctgct ggaacatctg 550

catcccttcc tgcagaggca gcagctggat tatggcatct acgtcatcca 600

ccaggctgaa ggtaaaaagt ttaatcgagc caaactcttg aatgtgggct 650

atctagaagc cctcaaggaa gaaaattggg actgctttat attccacgat 700

gtggacctgg tacccgagaa tgactttaac ctttacaagt gtgaggagca 750

tcccaagcat ctggtggttg gcaggaacag cactgggtac aggttacgtt 800

acagtggata ttttgggggt gttactgccc taagcagaga gcagtttttc 850

aaggtgaatg gattctctaa caactactgg ggatggggag gcgaagacga 900

tgacctcaga ctcagggttg agctccaaag aatgaaaatt tcccggcccc 950

tgcctgaagt gggtaaatat acaatggtct tccacactag agacaaaggc 1000

aatgaggtga acgcagaacg gatgaagctc ttacaccaag tgtcacgagt 1050

ctggagaaca gatgggttga gtagttgttc ttataaatta gtatctgtgg 1100

aacacaatcc tttatatatc aacatcacag tggatttctg gtttggtgca 1150

tgaccctgga tcttttggtg atgtttggaa gaactgattc tttgtttgca 1200

ataattttgg cctagagact tcaaatagta gcacacatta agaacctgtt 1250

acagctcatt gttgagctga atttttcctt tttgtatttt cttagcagag 1300

ctcctggtga tgtagagtat aaaacagttg taacaagaca gctttcttag 1350

tcattttgat catgagggtt aaatattgta atatggatac ttgaaggact 1400

ttatataaaa ggatgactca aaggataaaa tgaacgctat ttgaggactc 1450

tggttgaagg agatttattt aaatttgaag taatatatta tgggataaaa 1500

ggccacagga aataagactg ctgaatgtct gagagaacca gagttgttct 1550

cgtccaaggt agaaaggtac gaagatacaa tactgttatt catttatcct 1600

gtacaatcat ctgtgaagtg gtggtgtcag gtgagaaggc gtccacaaaa 1650

gaggggagaa aaggcgacga atcaggacac agtgaacttg ggaatgaaga 1700

ggtagcagga gggtggagtg tcggctgcaa aggcagcagt agctgagctg 1750

gttgcaggtg ctgatagcct tcaggggagg acctgcccag gtatgccttc 1800

cagtgatgcc caccagagaa tacattctct attagttttt aaagagtttt 1850

tgtaaaatga ttttgtacaa gtaggatatg aattagcagt ttacaagttt 1900

acatattaac taataataaa tatgtctatc aaatacctct gtagtaaaat 1950

gtgaaaaagc aaaa 1964

<210> 236
<211> 344
<212> PRT
<213> Homo sapiens

<220>
<221> Signal peptide
<222> 1-27
<223> Signal peptide

<220>
<221> N-glycosylation sites
<222> 4-7, 220-223, 335-338
<223> N-glycosylation sites

<220>
<221> Xylose isomerase proteins
<222> 191-201
<223> Xylose isomerase proteins

<400> 236
Met Gly Phe Asn Leu Thr Phe His Leu Ser Tyr Lys Phe Arg Leu
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Leu Leu Leu Leu Thr Leu Cys Leu Thr Val Val Gly Trp Ala Thr
20 25 30

Ser Asn Tyr Phe Val Gly Ala Ile Gln Glu Ile Pro Lys Ala Lys
35 40 45

Glu Phe Met Ala Asn Phe His Lys Thr Leu Ile Leu Gly Lys Gly
50 55 60

Lys Thr Leu Thr Asn Glu Ala Ser Thr Lys Lys Val Glu Leu Asp
65 70 75

Asn Cys Pro Ser Val Ser Pro Tyr Leu Arg Gly Gln Ser Lys Leu
80 85 90

Ile Phe Lys Pro Asp Leu Thr Leu Glu Glu Val Gln Ala Glu Asn
95 100 105

Pro Lys Val Ser Arg Gly Arg Tyr Arg Pro Gln Glu Cys Lys Ala
110 115 120

Leu Gln Arg Val Ala Ile Leu Val Pro His Arg Asn Arg Glu Lys
125 130 135

His Leu Met Tyr Leu Leu Glu His Leu His Pro Phe Leu Gln Arg
140 145 150

Gln Gln Leu Asp Tyr Gly Ile Tyr Val Ile His Gln Ala Glu Gly
155 160 165

Lys Ly's Phe Asn Arg Ala Lys Leu Leu Asn Val Gly Tyr Leu Glu
170 175 180

Ala Leu Lys Glu Glu Asn Trp Asp Cys Phe Ile Phe His Asp Val
185 190 195

Asp Leu Val Pro Glu Asn Asp Phe Asn Leu Tyr Lys Cys Glu Glu
200 205 210

His Pro Lys His Leu Val Val Gly Arg Asn Ser Thr Gly Tyr Arg
215 220 225

Leu Arg Tyr Ser Gly Tyr Phe Gly Gly Val Thr Ala Leu Ser Arg
230 235 240

Glu Gln Phe Phe Lys Val Asn Gly Phe Ser Asn Asn Tyr Trp Gly
245 250 255

Trp Gly Gly Glu Asp Asp Asp Leu Arg Leu Arg Val Glu Leu Gln
260 265 270

Arg Met Lys Ile Ser Arg Pro Leu Pro Glu Val Gly Lys Tyr Thr
275 280 285

Met Val Phe His Thr Arg Asp Lys Gly Asn Glu Val Asn Ala Glu
290 295 300

Arg Met Lys Leu Leu His Gln Val Ser Arg Val Trp Arg Thr Asp
305 310 315

Gly Leu Ser Ser Cys Ser Tyr Lys Leu Val Ser Val Glu His Asn
320 325 330

Pro Leu Tyr Ile Asn Ile Thr Val Asp Phe Trp Phe Gly Ala
335 340

<210> 237
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 237
ccttacctca gaggccagag caagc 25

<210> 238
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 238
gagcttcatc cgttctgcgt tcacc 25

<210> 239
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 239
caggaatgta aagctttaca gagggtcgcc atcctcgttc cccacc 46

<210> 240
<211> 2567
<212> DNA
<213> Homo sapiens

<400> 240
cgtgggccgg ggtcgcgcag cgggctgtgg gcgcgcccgg aggagcgacc 50

gccgcagttc tcgagctcca gctgcattcc ctccgcgtcc gccccacgct 100

tctcccgctc cgggccccgc aatggcccag gcagtgtggt cgcgcctcgg 150

ccgcatcctc tggcttgcct gcctcctgcc ctgggccccg gcaggggtgg 200

ccgcaggcct gtatgaactc aatctcacca ccgatagccc tgccaccacg 250

ggagcggtgg tgaccatctc ggccagcctg gtggccaagg acaacggcag 300

cctggccctg cccgctgacg cccacctcta ccgcttccac tggatccaca 350

ccccgctggt gcttactggc aagatggaga agggtctcag ctccaccatc 400

cgtgtggtcg gccacgtgcc cggggaattc ccggtctctg tctgggtcac 450

tgccgctgac tgctggatgt gccagcctgt ggccaggggc tttgtggtcc 500

tccccatcac agagttcctc gtgggggacc ttgttgtcac ccagaacact 550

tccctaccct ggcccagctc ctatctcact aagaccgtcc tgaaagtctc 600

cttcctcctc cacgacccga gcaacttcct caagaccgcc ttgtttctct 650

acagctggga cttcggggac gggacccaga tggtgactga agactccgtg 700

gtctattata actattccat catcgggacc ttcaccgtga agctcaaagt 750

ggtggcggag tgggaagagg tggagccgga tgccacgagg gctgtgaagc 800

agaagaccgg ggacttctcc gcctcgctga agctgcagga aacccttcga 850

ggcatccaag tgttggggcc caccctaatt cagaccttcc aaaagatgac 900

cgtgaccttg aacttcctgg ggagccctcc tctgactgtg tgctggcgtc 950

tcaagcctga gtgcctcccg ctggaggaag gggagtgcca ccctgtgtcc 1000

gtggccagca cagcgtacaa cctgacccac accttcaggg accctgggga 1050

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accacaagat ccaggtgtgg ccctccagaa tccagccggc tgtctttgct 1150

ttcccatgtg ctacacttat cactgtgatg ttggccttca tcatgtacat 1200

gaccctgcgg aatgccactc agcaaaagga catggtggag aacccggagc 1250

caccctctgg ggtcaggtgc tgctgccaga tgtgctgtgg gcctttcttg 1300

ctggagactc catctgagta cctggaaatt gttcgtgaga accacgggct 1350

gctcccgccc ctctataagt ctgtcaaaac ttacaccgtg tgagcactcc 1400

ccctccccac cccatctcag tgttaactga ctgctgactt ggagtttcca 1450

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ttggcctgga tcatccatcc atctgtacag ttcagccact gccacaagcc 1550

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cagccactga cataagcccc actcggttac caccccccttg acccccctacc 1650

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gtgccagaga gctagaaaga aggtcataaa gggttaaaaa tccataacta 1850

aaggttgtac acatagatgg gcacactcac agagagaagt gtgcatgtac 1900

acacaccaca cacacacaca cacacacaca cacagaaata taaacacatg 1950

cgtcacatgg gcatttcaga tgatcagctc tgtatctggt taagtcggtt 2000

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gccctgacag gttctgggcc cgggccctcc ctttgtgctt tgtctctgca 2100

gttcttgcgc cctttataag gccatcctag tccctgctgg ctggcagggg 2150

cctggatggg gggcaggact aatactgagt gattgcagag tgctttataa 2200

atatcacctt attttatcga aacccatctg tgaaactttc actgaggaaa 2250

aggccttgca gcggtagaag aggttgagtc aaggccgggc gcggtggctc 2300

acgcctgtaa tcccagcact ttgggaggcc gaggcgggtg gatcacgaga 2350

tcaggagatc gagaccaccc tggctaacac ggtgaaaccc cgtctctact 2400

aaaaaaatac aaaaagttag ccgggcgtgg tggtgggtgc ctgtagtccc 2450

agctactcgg gaggctgagg caggagaatg gtgcgaaccc gggaggcgga 2500

gcttgcagtg agcccagatg gcgccactgc actccagcct gagtgacaga 2550

gcgagactct gtctcca 2567

<210> 241
<211> 423
<212> PRT
<213> Homo sapiens

<400> 241

Met	Ala	Gln	Ala	Val	Trp	Ser	Arg	Leu	Gly	Arg	Ile	Leu	Trp	Leu	
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Ala	Cys	Leu	Leu	Pro	Trp	Ala	Pro	Ala	Gly	Val	Ala	Ala	Gly	Leu	
				20				25						30	
Tyr	Glu	Leu	Asn	Leu	Thr	Thr	Asp	Ser	Pro	Ala	Thr	Thr	Gly	Ala	
				35				40						45	
Val	Val	Thr	Ile	Ser	Ala	Ser	Leu	Val	Ala	Lys	Asp	Asn	Gly	Ser	
				50				55						60	
Leu	Ala	Leu	Pro	Ala	Asp	Ala	His	Leu	Tyr	Arg	Phe	His	Trp	Ile	
				65				70						75	
His	Thr	Pro	Leu	Val	Leu	Thr	Gly	Lys	Met	Glu	Lys	Gly	Leu	Ser	
				80				85						90	
Ser	Thr	Ile	Arg	Val	Val	Gly	His	Val	Pro	Gly	Glu	Phe	Pro	Val	
				95				100						105	
Ser	Val	Trp	Val	Thr	Ala	Ala	Asp	Cys	Trp	Met	Cys	Gln	Pro	Val	
				110				115						120	
Ala	Arg	Gly	Phe	Val	Val	Leu	Pro	Ile	Thr	Glu	Phe	Leu	Val	Gly	
				125				130						135	
Asp	Leu	Val	Val	Thr	Gln	Asn	Thr	Ser	Leu	Pro	Trp	Pro	Ser	Ser	
				140				145						150	
Tyr	Leu	Thr	Lys	Thr	Val	Leu	Lys	Val	Ser	Phe	Leu	Leu	His	Asp	
				155				160						165	
Pro	Ser	Asn	Phe	Leu	Lys	Thr	Ala	Leu	Phe	Leu	Tyr	Ser	Trp	Asp	
				170				175						180	
Phe	Gly	Asp	Gly	Thr	Gln	Met	Val	Thr	Glu	Asp	Ser	Val	Val	Tyr	
				185				190						195	

Tyr Asn Tyr Ser Ile Ile Gly Thr Phe Thr Val Lys Leu Lys Val
200 205 210

Val Ala Glu Trp Glu Glu Val Glu Pro Asp Ala Thr Arg Ala Val
215 220 225

Lys Gln Lys Thr Gly Asp Phe Ser Ala Ser Leu Lys Leu Gln Glu
230 235 240

Thr Leu Arg Gly Ile Gln Val Leu Gly Pro Thr Leu Ile Gln Thr
245 250 255

Phe Gln Lys Met Thr Val Thr Leu Asn Phe Leu Gly Ser Pro Pro
260 265 270

Leu Thr Val Cys Trp Arg Leu Lys Pro Glu Cys Leu Pro Leu Glu
275 280 285

Glu Gly Glu Cys His Pro Val Ser Val Ala Ser Thr Ala Tyr Asn
290 295 300

Leu Thr His Thr Phe Arg Asp Pro Gly Asp Tyr Cys Phe Ser Ile
305 310 315

Arg Ala Glu Asn Ile Ile Ser Lys Thr His Gln Tyr His Lys Ile
320 325 330

Gln Val Trp Pro Ser Arg Ile Gln Pro Ala Val Phe Ala Phe Pro
335 340 345

Cys Ala Thr Leu Ile Thr Val Met Leu Ala Phe Ile Met Tyr Met
350 355 360

Thr Leu Arg Asn Ala Thr Gln Gln Lys Asp Met Val Glu Asn Pro
365 370 375

Glu Pro Pro Ser Gly Val Arg Cys Cys Cys Gln Met Cys Cys Gly
380 385 390

Pro Phe Leu Leu Glu Thr Pro Ser Glu Tyr Leu Glu Ile Val Arg
395 400 405

Glu Asn His Gly Leu Leu Pro Pro Leu Tyr Lys Ser Val Lys Thr
410 415 420

Tyr Thr Val

<210> 242
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 242
catttcctta ccctggaccc agctcc 26

<210> 243
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 243
gaaaggccca cagcacatct ggcag 25

<210> 244
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 244
ccacgacccg agcaacttcc tcaagaccga cttgtttctc tacagc 46

<210> 245
<211> 485
<212> DNA
<213> Homo sapiens

<400> 245
gctcaagacc cagcagtggg acagccagac agacggcacg atggcactga 50

gctcccagat ctgggccgct tgcctcctgc tcctcctcct cctcgccagc 100

ctgaccagtg gctctgtttt cccacaacag acgggacaac ttgcagagct 150

gcaaccccag gacagagctg gagccagggc cagctggatg cccatgttcc 200

agaggcgaag gaggcgagac acccacttcc ccatctgcat tttctgctgc 250

ggctgctgtc atcgatcaaa gtgtgggatg tgctgcaaga cgtagaacct 300

acctgccctg cccccgtccc ctcccttcct tatttattcc tgctgcccca 350

gaacataggt cttggaataa aatggctggt tcttttgttt tccaaaaaaa 400

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 485

<210> 246
<211> 84
<212> PRT
<213> Homo sapiens

<400> 246
Met Ala Leu Ser Ser Gln Ile Trp Ala Ala Cys Leu Leu Leu Leu
1 5 10 15

Leu Leu Leu Ala Ser Leu Thr Ser Gly Ser Val Phe Pro Gln Gln
20 25 30

Thr Gly Gln Leu Ala Glu Leu Gln Pro Gln Asp Arg Ala Gly Ala
35 40 45

Arg Ala Ser Trp Met Pro Met Phe Gln Arg Arg Arg Arg Arg Asp
50 55 60

Thr His Phe Pro Ile Cys Ile Phe Cys Cys Gly Cys Cys His Arg
65 70 75

Ser Lys Cys Gly Met Cys Cys Lys Thr
80

<210> 247
<211> 2359
<212> DNA
<213> Homo sapiens

<400> 247
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tgctggcctg gcctggatct tccaccatgt tcctgttgct gcctttttgat 100

agcctgattg tcaaccttct gggcatctcc ctgactgtcc tcttcaccct 150

ccttctcgtt ttcatcatag tgccagccat ttttggagtc tcctttggta 200

tccgcaaact ctacatgaaa agtctgttaa aaatctttgc gtgggctacc 250

ttgagaatgg agcgaggagc caaggagaag aaccaccagc tttacaagcc 300

ctacaccaac ggaatcattg caaaggatcc cacttcacta gaagaagaga 350

tcaaagagat tcgtcgaagt ggtagtagta aggctctgga caacactcca 400

gagttcgagc tctctgacat tttctacttt tgccggaaag gaatggagac 450

cattatggat gatgaggtga caaagagatt ctcagcagaa gaactggagt 500

cctggaacct gctgagcaga accaattata acttccagta catcagcctt 550

cggctcacgg tcctgtgggg gttaggagtg ctgattcggt actgctttct 600

gctgccgctc aggatagcac tggctttcac agggattagc cttctggtgg 650

tgggcacaac tgtggtggga tacttgccaa atgggaggtt taaggaattc 700

atgagtaaac atgttcactt aatgtgttac cggatctgcg tgcgagcgct 750

gacagccatc atcacctacc atgacaggga aaacagacca agaaatggtg 800

gcatctgtgt ggccaatcat acctcaccga tcgatgtgat catcttggcc 850

agcgatggct attatgccat ggtgggtcaa gtgcacgggg gactcatggg 900

tgtgattcag agagccatgg tgaaggcctg cccacacgtc tggtttgagc 950

gctcggaagt gaaggatcgc cacctggtgg ctaagagact gactgaacat 1000

gtgcaagata aaagcaagct gcctatcctc atcttcccag aaggaacctg 1050

catcaataat acatcggtga tgatgttcaa aaagggaagt tttgaaattg 1100

gagccacagt ttaccctgtt gctatcaagt atgaccctca atttggcgat 1150

gccttctgga acagcagcaa atacgggatg gtgacgtacc tgctgcgaat 1200

gatgaccagc tgggccattg tctgcagcgt gtggtacctg cctcccatga 1250

ctagagaggc agatgaagat gctgtccagt ttgcgaatag ggtgaaatct 1300

gccattgcca ggcagggagg acttgtggac ctgctgtggg atgggggcct 1350

gaagagggag aaggtgaagg acacgttcaa ggaggagcag cagaagctgt 1400

acagcaagat gatcgtgggg aaccacaagg acaggagccg ctcctgagcc 1450

tgcctccagc tggctggggc caccgtgcgg ggtgccaacg ggctcagagc 1500

tggagttgcc gccgccgccc ccactgctgt gtcctttcca gactccaggg 1550

ctccccgggc tgctctggat cccaggactc cggctttcgc cgagccgcag 1600

cgggatccct gtgcacccgg cgcagcctac ccttggtggt ctaaacggat 1650

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agtcgttgga ggaatgccat taaagtgaac tccccacctt tgcacgctgt 1750

gcgggctgag tggttgggga gatgtggcca tggtcttgtg ctagagatgg 1800

cggtacaaga gtctgttatg caagcccgtg tgccagggat gtgctggggg 1850

cggccacccg ctctccagga aaggcacagc tgaggcactg tggctggctt 1900

cggcctcaac atcgccccca gccttggagc tctgcagaca tgataggaag 1950

gaaactgtca tctgcagggg ctttcagcaa aatgaagggt tagattttta 2000

tgctgctgct gatggggtta ctaaagggag gggaagaggc caggtgggcc 2050

gctgactggg ccatggggag aacgtgtgtt cgtactccag gctaaccctg 2100

aactccccat gtgatgcgcg ctttgttgaa tgtgtgtctc ggtttcccca 2150

tctgtaatat gagtcggggg gaatggtggt gattcctacc tcacagggct 2200

gttgtgggga ttaaagtgct gcgggtgagt gaaggacaca tcacgttcag 2250

tgtttcaagt acaggcccac aaaacggggc acggcaggcc tgagctcaga 2300

gctgctgcac tgggctttgg atttgttctt gtgagtaaat aaaactggct 2350

ggtgaatga 2359

<210> 248
<211> 456
<212> PRT
<213> Homo sapiens

<400> 248

Met	Phe	Leu	Leu	Leu	Pro	Phe	Asp	Ser	Leu	Ile	Val	Asn	Leu	Leu	
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Gly	Ile	Ser	Leu	Thr	Val	Leu	Phe	Thr	Leu	Leu	Leu	Val	Phe	Ile	
				20				25						30	
Ile	Val	Pro	Ala	Ile	Phe	Gly	Val	Ser	Phe	Gly	Ile	Arg	Lys	Leu	
				35				40						45	
Tyr	Met	Lys	Ser	Leu	Leu	Lys	Ile	Phe	Ala	Trp	Ala	Thr	Leu	Arg	
				50				55						60	
Met	Glu	Arg	Gly	Ala	Lys	Glu	Lys	Asn	His	Gln	Leu	Tyr	Lys	Pro	
				65				70						75	

Tyr Thr Asn Gly Ile Ile Ala Lys Asp Pro Thr Ser Leu Glu Glu
80 85 90

Glu Ile Lys Glu Ile Arg Arg Ser Gly Ser Ser Lys Ala Leu Asp
95 100 105

Asn Thr Pro Glu Phe Glu Leu Ser Asp Ile Phe Tyr Phe Cys Arg
110 115 120

Lys Gly Met Glu Thr Ile Met Asp Asp Glu Val Thr Lys Arg Phe
125 130 135

Ser Ala Glu Glu Leu Glu Ser Trp Asn Leu Leu Ser Arg Thr Asn
140 145 150

Tyr Asn Phe Gln Tyr Ile Ser Leu Arg Leu Thr Val Leu Trp Gly
155 160 165

Leu Gly Val Leu Ile Arg Tyr Cys Phe Leu Leu Pro Leu Arg Ile
170 175 180

Ala Leu Ala Phe Thr Gly Ile Ser Leu Leu Val Val Gly Thr Thr
185 190 195

Val Val Gly Tyr Leu Pro Asn Gly Arg Phe Lys Glu Phe Met Ser
200 205 210

Lys His Val His Leu Met Cys Tyr Arg Ile Cys Val Arg Ala Leu
215 220 225

Thr Ala Ile Ile Thr Tyr His Asp Arg Glu Asn Arg Pro Arg Asn
230 235 240

Gly Gly Ile Cys Val Ala Asn His Thr Ser Pro Ile Asp Val Ile
245 250 255

Ile Leu Ala Ser Asp Gly Tyr Tyr Ala Met Val Gly Gln Val His
260 265 270

Gly Gly Leu Met Gly Val Ile Gln Arg Ala Met Val Lys Ala Cys
275 280 285

Pro His Val Trp Phe Glu Arg Ser Glu Val Lys Asp Arg His Leu
290 295 300

Val Ala Lys Arg Leu Thr Glu His Val Gln Asp Lys Ser Lys Leu
305 310 315

Pro Ile Leu Ile Phe Pro Glu Gly Thr Cys Ile Asn Asn Thr Ser
320 325 330

Val Met Met Phe Lys Lys Gly Ser Phe Glu Ile Gly Ala Thr Val
335 340 345

Tyr Pro Val Ala Ile Lys Tyr Asp Pro Gln Phe Gly Asp Ala Phe
350 355 360

Trp Asn Ser Ser Lys Tyr Gly Met Val Thr Tyr Leu Leu Arg Met
365 370 375

Met Thr Ser Trp Ala Ile Val Cys Ser Val Trp Tyr Leu Pro Pro
380 385 390

Met Thr Arg Glu Ala Asp Glu Asp Ala Val Gln Phe Ala Asn Arg
395 400 405

Val Lys Ser Ala Ile Ala Arg Gln Gly Gly Leu Val Asp Leu Leu
410 415 420

Trp Asp Gly Gly Leu Lys Arg Glu Lys Val Lys Asp Thr Phe Lys
425 430 435

Glu Glu Gln Gln Lys Leu Tyr Ser Lys Met Ile Val Gly Asn His
440 445 450

Lys Asp Arg Ser Arg Ser
455

<210> 249
<211> 1103
<212> DNA
<213> Homo sapiens

<400> 249
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gccctcggca gcctcggcct ccacacctgg caggcccagg ctgttcccac 150

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gttgtgcaga ggagatggag gagaaggcag ccccccctgct aaaggaggaa 250

atggcccacc atgccctgct gcgggaatcc tgggaggcag cccaggagac 300

ctgggaggac aagcgtcgag ggcttacctt gccccctggc ttcaaagccc 350

agaatggaat agccattatg gtctacacca actcatcgaa caccttgtac 400

tgggagttga atcaggccgt gcggacgggc ggaggctccc gggagctcta 450

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gtgttccgag gtgtgggcag ccttcgcttt gaacccaaga ggctggggga 600

ctctgtccgc ttgggccagt ttgcctccag ctccctggat aaggcagtgg 650

cccacagatt tggggagaag aggcggggct gtgtgtctgc gccaggggtg 700

cagctagggt cacaatctga gggggcctcc tctctgcccc cctggaagac 750

tctgctcttg gcccctggag agttccagct ctcaggggtt gggccctgaa 800

agtccaacat ctgccactta ggagccctgg gaacgggtga ccttcatatg 850

acgaagaggc acctccagca gccttgagaa gcaagaacat ggttccggac 900

ccagccctag cagccttctc cccaaccagg atgttggcct ggggaggcca 950

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caaggaaagt actgaggcag ccacttgatt gaacggtgtt gcaatgtgga 1050

EP 2 272 963 A2

gacatggagt tttattgagg tagctacgtg attaaatggt attgcagtgt 1100

gga 1103

<210> 250
<211> 240
<212> PRT
<213> Homo sapiens

<400> 250

Met	Ala	Leu	Ala	Ala	Leu	Met	Ile	Ala	Leu	Gly	Ser	Leu	Gly	Leu	
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His	Thr	Trp	Gln	Ala	Gln	Ala	Val	Pro	Thr	Ile	Leu	Pro	Leu	Gly	
				20				25						30	
Leu	Ala	Pro	Asp	Thr	Phe	Asp	Asp	Thr	Tyr	Val	Gly	Cys	Ala	Glu	
				35				40						45	
Glu	Met	Glu	Glu	Lys	Ala	Ala	Pro	Leu	Leu	Lys	Glu	Glu	Met	Ala	
				50				55						60	
His	His	Ala	Leu	Leu	Arg	Glu	Ser	Trp	Glu	Ala	Ala	Gln	Glu	Thr	
				65				70						75	
Trp	Glu	Asp	Lys	Arg	Arg	Gly	Leu	Thr	Leu	Pro	Pro	Gly	Phe	Lys	
				80				85						90	
Ala	Gln	Asn	Gly	Ile	Ala	Ile	Met	Val	Tyr	Thr	Asn	Ser	Ser	Asn	
				95				100						105	
Thr	Leu	Tyr	Trp	Glu	Leu	Asn	Gln	Ala	Val	Arg	Thr	Gly	Gly	Gly	
				110				115						120	
Ser	Arg	Glu	Leu	Tyr	Met	Arg	His	Phe	Pro	Phe	Lys	Ala	Leu	His	
				125				130						135	
Phe	Tyr	Leu	Ile	Arg	Ala	Leu	Gln	Leu	Leu	Arg	Gly	Ser	Gly	Gly	
				140				145						150	
Cys	Ser	Arg	Gly	Pro	Gly	Glu	Val	Val	Phe	Arg	Gly	Val	Gly	Ser	
				155				160						165	
Leu	Arg	Phe	Glu	Pro	Lys	Arg	Leu	Gly	Asp	Ser	Val	Arg	Leu	Gly	
				170				175						180	
Gln	Phe	Ala	Ser	Ser	Ser	Leu	Asp	Lys	Ala	Val	Ala	His	Arg	Phe	
				185				190						195	
Gly	Glu	Lys	Arg	Arg	Gly	Cys	Val	Ser	Ala	Pro	Gly	Val	Gln	Leu	
				200				205						210	
Gly	Ser	Gln	Ser	Glu	Gly	Ala	Ser	Ser	Leu	Pro	Pro	Trp	Lys	Thr	
				215				220						225	
Leu	Leu	Leu	Ala	Pro	Gly	Glu	Phe	Gln	Leu	Ser	Gly	Val	Gly	Pro	
				230				235						240	

<210> 251
<211> 50
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synthetic oligonucleotide probe

<400> 251
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<210> 252
<211> 1076
<212> DNA
<213> Homo sapiens

<400> 252
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gcctctggac ccgtgaaaga gctggtcggt tccgttggtg gggccgtgac 150

tttccccctg aagtccaaag taaagcaagt tgactctatt gtctggacct 200

tcaacacaac ccctcttgtc accatacagc cagaaggggg cactatcata 250

gtgacccaaa atcgtaatag ggagagagta gacttcccag atggaggcta 300

ctccctgaag ctcagcaaac tgaagaagaa tgactcaggg atctactatg 350

tggggatata cagctcatca ctccagcagc cctccaccca ggagtacgtg 400

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gagcaataag aatggcacct gtgtgaccaa tctgacatgc tgcatggaac 500

atggggaaga ggatgtgatt tatacctgga aggccctggg gcaagcagcc 550

aatgagtccc ataatgggtc catcctcccc atctcctgga gatggggaga 600

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tctcaagccc catccttgcc aggaagctct gtgaaggtgc tgctgatgac 700

ccagattcct ccatggtcct cctgtgtctc ctgttggtgc ccctcctgct 750

cagtctcttt gtactggggc tatttctttg gtttctgaag agagagagac 800

aagaagagta cattgaagag aagaagagag tggacatttg tcgggaaact 850

cctaacatat gcccccattc tggagagaac acagagtacg acacaatccc 900

tcacactaat agaacaatcc taaaggaaga tccagcaaat acggtttact 950

ccactgtgga aataccgaaa aagatggaaa atccccactc actgctcacg 1000

atgccagaca caccaaggct atttgcctat gagaatgtta tctagacagc 1050

agtgcactcc cctaagtctc tgctca 1076

<210> 253
<211> 335
<212> PRT
<213> Homo sapiens

<400> 253
Met Ala Gly Ser Pro Thr Cys Leu Thr Leu Ile Tyr Ile Leu Trp

FORM PCT/GB2005/050

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Gln Leu Thr Gly Ser Ala Ala Ser Gly Pro Val Lys Glu Leu Val
                20                  25                  30

Gly Ser Val Gly Gly Ala Val Thr Phe Pro Leu Lys Ser Lys Val
                35                  40                  45

Lys Gln Val Asp Ser Ile Val Trp Thr Phe Asn Thr Thr Pro Leu
                50                  55                  60

Val Thr Ile Gln Pro Glu Gly Gly Thr Ile Ile Val Thr Gln Asn
                65                  70                  75

Arg Asn Arg Glu Arg Val Asp Phe Pro Asp Gly Gly Tyr Ser Leu
                80                  85                  90

Lys Leu Ser Lys Leu Lys Lys Asn Asp Ser Gly Ile Tyr Tyr Val
                95                 100                 105

Gly Ile Tyr Ser Ser Ser Leu Gln Gln Pro Ser Thr Gln Glu Tyr
               110                 115                 120

Val Leu His Val Tyr Glu His Leu Ser Lys Pro Lys Val Thr Met
               125                 130                 135

Gly Leu Gln Ser Asn Lys Asn Gly Thr Cys Val Thr Asn Leu Thr
               140                 145                 150

Cys Cys Met Glu His Gly Glu Glu Asp Val Ile Tyr Thr Trp Lys
               155                 160                 165

Ala Leu Gly Gln Ala Ala Asn Glu Ser His Asn Gly Ser Ile Leu
               170                 175                 180

Pro Ile Ser Trp Arg Trp Gly Glu Ser Asp Met Thr Phe Ile Cys
               185                 190                 195

Val Ala Arg Asn Pro Val Ser Arg Asn Phe Ser Ser Pro Ile Leu
               200                 205                 210

Ala Arg Lys Leu Cys Glu Gly Ala Ala Asp Asp Pro Asp Ser Ser
               215                 220                 225

Met Val Leu Leu Cys Leu Leu Leu Val Pro Leu Leu Leu Ser Leu
               230                 235                 240

Phe Val Leu Gly Leu Phe Leu Trp Phe Leu Lys Arg Glu Arg Gln
               245                 250                 255

Glu Glu Tyr Ile Glu Glu Lys Lys Arg Val Asp Ile Cys Arg Glu
               260                 265                 270

Thr Pro Asn Ile Cys Pro His Ser Gly Glu Asn Thr Glu Tyr Asp
               275                 280                 285

Thr Ile Pro His Thr Asn Arg Thr Ile Leu Lys Glu Asp Pro Ala
               290                 295                 300

Asn Thr Val Tyr Ser Thr Val Glu Ile Pro Lys Lys Met Glu Asn
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Pro His Ser Leu Leu Thr Met Pro Asp Thr Pro Arg Leu Phe Ala
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320 325 330

Tyr Glu Asn Val Ile
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<210> 254
<211> 1053
<212> DNA
<213> Homo sapiens

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ggccgtgact ttccccctga agtccaaagt aaagcaagtt gactctattg 150

tctggacctt caacacaacc cctcttgtca ccatacagcc agaaggggge 200

actatcatag tgacccaaaa tcgtaatagg gagagagtag acttcccaga 250

tggaggctac tccctgaagc tcagcaaact gaagaagaat gactcaggga 300

tctactatgt ggggatatac agctcatcac tccagcagcc ctccacccag 350

gagtacgtgc tgcatgtcta cgagcacctg tcaaagccta aagtcaccat 400

gggtctgcag agcaataaga atggcacctg tgtgaccaat ctgacatgct 450

gcatggaaca tggggaagag gatgtgattt atacctggaa ggccctgggg 500

caagcagcca atgagtccca taatgggtcc atcctcccca tctcctggag 550

atggggagaa agtgatatga ccttcatctg cgttgccagg aaccctgtca 600

gcagaaactt ctcaagcccc atccttgcca ggaagctctg tgaaggtgct 650

gctgatgacc cagattcctc catggtcctc ctgtgtctcc tgttggtgcc 700

cctcctgctc agtctctttg tactggggct atttctttgg tttctgaaga 750

gagagagaca agaagagtac attgaagaga agaagagagt ggacatttgt 800

cgggaaactc ctaacatatg cccccattct ggagagaaca cagagtacga 850

cacaatccct cacactaata gaacaatcct aaaggaagat ccagcaaata 900

cggtttactc cactgtggaa ataccgaaaa agatggaaaa tccccactca 950

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aaa 1053

<210> 255
<211> 860
<212> DNA
<213> Homo sapiens

<400> 255
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gatgctgctg ctgctgtgtt tgggactgac cctagtctgt gtccatgcag 100

aagaagctag ttctacggga aggaacttta atgtagaaaa gattaatggg 150

gaatggcata ctattatcct ggcctctgac aaaagagaaa agatagaaga 200

acatggcaac tttagacttt ttctggagca aatccatgtc ttggagaatt 250

ccttagttct taaagtccat actgtaagag atgaagagtg ctccgaatta 300

tctatggttg ctgacaaaac agaaaaggct ggtgaatatt ctgtgacgta 350

tgatggattc aatacattta ctatacctaa gacagactat gataactttc 400

ttatggctca cctcattaac gaaaaggatg gggaaacctt ccagctgatg 450

gggctctatg gccgagaacc agatttgagt tcagacatca aggaaaggtt 500

tgcacaacta tgtgaggagc atggaatcct tagagaaaat atcattgacc 550

tatccaatgc caatcgctgc ctccaggccc gagaatgaag aatggcctga 600

gcctccagtg ttgagtggac acttctcacc aggactccac catcatccct 650

tcctatccat acagcatccc cagtataaat tctgtgatct gcattccatc 700

ctgtctcact gagaagtcca attccagtct atcaacatgt tacctaggat 750

acctcatcaa gaatcaaaga cttctttaaa tttctctttg atacaccctt 800

gacaattttt catgaaatta ttcctcttcc tgttcaataa atgattaccc 850

ttgcacttaa 860

<210> 256
<211> 180
<212> PRT
<213> Homo sapiens

<400> 256

Met	Lys	Met	Leu	Leu	Leu	Leu	Cys	Leu	Gly	Leu	Thr	Leu	Val	Cys	
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Val	His	Ala	Glu	Glu	Ala	Ser	Ser	Thr	Gly	Arg	Asn	Phe	Asn	Val	
				20				25						30	
Glu	Lys	Ile	Asn	Gly	Glu	Trp	His	Thr	Ile	Ile	Leu	Ala	Ser	Asp	
				35				40						45	
Lys	Arg	Glu	Lys	Ile	Glu	Glu	His	Gly	Asn	Phe	Arg	Leu	Phe	Leu	
				50				55						60	
Glu	Gln	Ile	His	Val	Leu	Glu	Asn	Ser	Leu	Val	Leu	Lys	Val	His	
				65				70						75	
Thr	Val	Arg	Asp	Glu	Glu	Cys	Ser	Glu	Leu	Ser	Met	Val	Ala	Asp	
				80				85						90	
Lys	Thr	Glu	Lys	Ala	Gly	Glu	Tyr	Ser	Val	Thr	Tyr	Asp	Gly	Phe	
				95				100						105	
Asn	Thr	Phe	Thr	Ile	Pro	Lys	Thr	Asp	Tyr	Asp	Asn	Phe	Leu	Met	
				110				115						120	

Ala His Leu Ile Asn Glu Lys Asp Gly Glu Thr Phe Gln Leu Met
125 130 135

Gly Leu Tyr Gly Arg Glu Pro Asp Leu Ser Ser Asp Ile Lys Glu
140 145 150

Arg Phe Ala Gln Leu Cys Glu Glu His Gly Ile Leu Arg Glu Asn
155 160 165

Ile Ile Asp Leu Ser Asn Ala Asn Arg Cys Leu Gln Ala Arg Glu
170 175 180

<210> 257
<211> 766
<212> DNA
<213> Homo sapiens

<400> 257
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gacatcctgc aatggattca gcctgctggt tctactgctg ttaggagtag 100

ttctcaatgc gatacctcta attgtcagct tagttgagga agaccaattt 150

tctcaaaacc ccatctcttg ctttgagtgg tggttcccag gaattatagg 200

agcaggtctg atggccattc cagcaacaac aatgtccttg acagcaagaa 250

aaagagcgtg ctgcaacaac agaactggaa tgtttctttc atcatttttc 300

agtgtgatca cagtcattgg tgctctgtat tgcatgctga tatccatcca 350

ggctctctta aaaggtcctc tcatgtgtaa ttctccaagc aacagtaatg 400

ccaattgtga attttcattg aaaaacatca gtgacattca tccagaatcc 450

ttcaacttgc agtggttttt caatgactct tgtgcacctc ctactggttt 500

caataaaccc accagtaacg acaccatggc gagtggctgg agagcatcta 550

gtttccactt cgattctgaa gaaaacaaac ataggcttat ccacttctca 600

gtatttttag gtctattgct tgttggaatt ctggaggtcc tgtttgggct 650

cagtcagata gtcatcggtt tccttggctg tctgtgtgga gtctctaagc 700

gaagaagtca aattgtgtag tttaatggga ataaaatgta agtatcagta 750

gtttgaaaaa aaaaaa 766

<210> 258
<211> 229
<212> PRT
<213> Homo sapiens

<400> 258
Met Thr Cys Cys Glu Gly Trp Thr Ser Cys Asn Gly Phe Ser Leu
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Leu Val Leu Leu Leu Leu Gly Val Val Leu Asn Ala Ile Pro Leu
20 25 30

Ile Val Ser Leu Val Glu Glu Asp Gln Phe Ser Gln Asn Pro Ile

35 40 45

Ser Cys Phe Glu Trp Trp Phe Pro Gly Ile Ile Gly Ala Gly Leu
50 55 60

Met Ala Ile Pro Ala Thr Thr Met Ser Leu Thr Ala Arg Lys Arg
65 70 75

Ala Cys Cys Asn Asn Arg Thr Gly Met Phe Leu Ser Ser Phe Phe
80 85 90

Ser Val Ile Thr Val Ile Gly Ala Leu Tyr Cys Met Leu Ile Ser
95 100 105

Ile Gln Ala Leu Leu Lys Gly Pro Leu Met Cys Asn Ser Pro Ser
110 115 120

Asn Ser Asn Ala Asn Cys Glu Phe Ser Leu Lys Asn Ile Ser Asp
125 130 135

Ile His Pro Glu Ser Phe Asn Leu Gln Trp Phe Phe Asn Asp Ser
140 145 150

Cys Ala Pro Pro Thr Gly Phe Asn Lys Pro Thr Ser Asn Asp Thr
155 160 165

Met Ala Ser Gly Trp Arg Ala Ser Ser Phe His Phe Asp Ser Glu
170 175 180

Glu Asn Lys His Arg Leu Ile His Phe Ser Val Phe Leu Gly Leu
185 190 195

Leu Leu Val Gly Ile Leu Glu Val Leu Phe Gly Leu Ser Gln Ile
200 205 210

Val Ile Gly Phe Leu Gly Cys Leu Cys Gly Val Ser Lys Arg Arg
215 220 225

Ser Gln Ile Val

<210> 259
<211> 434
<212> DNA
<213> Homo sapiens

<400> 259
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caccatgagg ctgtcagtgt gtctcctgat ggtctcgctg gccctttgct 100

gctaccaggc ccatgctctt gtctgcccag ctgttgcttc tgagatcaca 150

gtcttcttat tcttaagtga cgctgcggta aacctccaag ttgccaaact 200

taatccacct ccagaagctc ttgcagccaa gttggaagtg aagcactgca 250

ccgatcagat atcttttaag aaacgactct cattgaaaaa gtcctggtgg 300

aaatagtgaa aaaatgtggt gtgtgacatg taaaaatgct caacctggtt 350

tccaaagtct ttcaacgaca ccctgatctt cactaaaaat tgtaaaggtt 400

tcaacacgtt gctttaataa atcacttgcc ctgc 434

<210> 260
<211> 83
<212> PRT
<213> Homo sapiens

<400> 260

Met	Arg	Leu	Ser	Val	Cys	Leu	Leu	Met	Val	Ser	Leu	Ala	Leu	Cys	
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Cys	Tyr	Gln	Ala	His	Ala	Leu	Val	Cys	Pro	Ala	Val	Ala	Ser	Glu	
				20				25						30	
Ile	Thr	Val	Phe	Leu	Phe	Leu	Ser	Asp	Ala	Ala	Val	Asn	Leu	Gln	
				35				40						45	
Val	Ala	Lys	Leu	Asn	Pro	Pro	Pro	Glu	Ala	Leu	Ala	Ala	Lys	Leu	
				50				55						60	
Glu	Val	Lys	His	Cys	Thr	Asp	Gln	Ile	Ser	Phe	Lys	Lys	Arg	Leu	
				65				70						75	
Ser	Leu	Lys	Lys	Ser	Trp	Trp	Lys								
				80											

<210> 261
<211> 636
<212> DNA
<213> Homo sapiens

<400> 261
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ctgaccaatt gagctgtgag cctggagcag atccgtgggc tgcagacccc 150

cgccccagtg cctctccccc tgcagccctg cccctcgaac tgtgacatgg 200

agagagtgac cctggccctt ctcctactgg caggcctgac tgccttggaa 250

gccaatgacc catttgccaa taaagacgat cccttctact atgactggaa 300

aaacctgcag ctgagcggac tgatctgcgg agggctcctg gccattgctg 350

ggatcgcggc agttctgagt ggcaaatgca aatacaagag cagccagaag 400

cagcacagtc ctgtacctga gaaggccatc ccactcatca ctccaggctc 450

tgccactact tgctgagcac aggactggcc tccagggatg gcctgaagcc 500

taacactggc ccccagcacc tcctcccctg ggaggcctta tcctcaagga 550

aggacttctc tccaagggca ggctgttagg ccccttttctg atcaggaggc 600

ttctttatga attaaactcg ccccaccacc ccctca 636

<210> 262
<211> 89
<212> PRT
<213> Homo sapiens

<400> 262
Met Glu Arg Val Thr Leu Ala Leu Leu Leu Leu Ala Gly Leu Thr
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Ala Leu Glu Ala Asn Asp Pro Phe Ala Asn Lys Asp Asp Pro Phe
20 25 30

Tyr Tyr Asp Trp Lys Asn Leu Gln Leu Ser Gly Leu Ile Cys Gly
35 40 45

Gly Leu Leu Ala Ile Ala Gly Ile Ala Ala Val Leu Ser Gly Lys
50 55 60

Cys Lys Tyr Lys Ser Ser Gln Lys Gln His Ser Pro Val Pro Glu
65 70 75

Lys Ala Ile Pro Leu Ile Thr Pro Gly Ser Ala Thr Thr Cys
80 85

<210> 263
<211> 1676
<212> DNA
<213> Homo sapiens

<400> 263
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ctgagcctgc cctggctggg cctcagaccg gtggcaatgt ccccatggct 100

actcctgctg ctggttgtgg gctcctggct actcgcccgc atcctggctt 150

ggacctatgc cttctataac aactgccgcc ggctccagtg tttcccacag 200

cccccaaaac ggaactggtt ttggggtcac ctgggcctga tcactcctac 250

agaggagggc ttgaaggact cgacccagat gtcggccacc tattcccagg 300

gctttacggt atggctgggt cccatcatcc ccttcatcgt tttatgccac 350

cctgacacca tccggtctat caccaatgcc tcagctgcca ttgcacccaa 400

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gccttccatt tcaacatcct gaagtcctat ataacgatct tcaacaagag 550

tgcaaacatc atgcttgaca agtggcagca cctggcctca gagggcagca 600

gtcgtctgga catgtttgag cacatcagcc tcatgacctt ggacagtcta 650

cagaaatgca tcttcagctt tgacagccat tgtcaggaga ggcccagtga 700

atatattgcc accatcttgg agctcagtgc ccttgtagag aaaagaagcc 750

agcatatcct ccagcacatg gactttctgt attacctctc ccatgacggg 800

cggcgcttcc acagggcctg ccgcctggtg catgacttca cagacgctgt 850

catccgggag cggcgtcgca ccctccccac tcagggtatt gatgattttt 900

tcaaagacaa agccaagtcc aagactttgg atttcattga tgtgcttctg 950

ctgagcaagg atgaagatgg gaaggcattg tcagatgagg atataagagc 1000

agaggctgac accttcatgt ttggaggcca tgacaccacg gccagtggcc 1050

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tgcacttccg gttcctgcca gaccacactg agccccgcag gaagctggaa 1550

ttgatcatgc gcgccgaggg cgggctttgg ctgcgggtgg agcccctgaa 1600

tgtaggcttg cagtgacttt ctgacccatc cacctgtttt tttgcagatt 1650

gtcatgaata aaacggtgct gtcaaa 1676

<210> 264
<211> 524
<212> PRT
<213> Homo sapiens

<400> 264

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Met	Ser	Pro	Trp	Leu	Leu	Leu	Leu	Leu	Val	Val	Gly	Ser	Trp	Leu	
			20					25						30	
Leu	Ala	Arg	Ile	Leu	Ala	Trp	Thr	Tyr	Ala	Phe	Tyr	Asn	Asn	Cys	
			35					40						45	
Arg	Arg	Leu	Gln	Cys	Phe	Pro	Gln	Pro	Pro	Lys	Arg	Asn	Trp	Phe	
			50					55						60	
Trp	Gly	His	Leu	Gly	Leu	Ile	Thr	Pro	Thr	Glu	Glu	Gly	Leu	Lys	
			65					70						75	
Asp	Ser	Thr	Gln	Met	Ser	Ala	Thr	Tyr	Ser	Gln	Gly	Phe	Thr	Val	
			80					85						90	
Trp	Leu	Gly	Pro	Ile	Ile	Pro	Phe	Ile	Val	Leu	Cys	His	Pro	Asp	
			95					100						105	
Thr	Ile	Arg	Ser	Ile	Thr	Asn	Ala	Ser	Ala	Ala	Ile	Ala	Pro	Lys	
			110					115						120	
Asp	Asn	Leu	Phe	Ile	Arg	Phe	Leu	Lys	Pro	Trp	Leu	Gly	Glu	Gly	
			125					130						135	

Ile Leu Leu Ser Gly Gly Asp Lys Trp Ser Arg His Arg Arg Met
140 145 150

Leu Thr Pro Ala Phe His Phe Asn Ile Leu Lys Ser Tyr Ile Thr
155 160 165

Ile Phe Asn Lys Ser Ala Asn Ile Met Leu Asp Lys Trp Gln His
170 175 180

Leu Ala Ser Glu Gly Ser Ser Arg Leu Asp Met Phe Glu His Ile
185 190 195

Ser Leu Met Thr Leu Asp Ser Leu Gln Lys Cys Ile Phe Ser Phe
200 205 210

Asp Ser His Cys Gln Glu Arg Pro Ser Glu Tyr Ile Ala Thr Ile
215 220 225

Leu Glu Leu Ser Ala Leu Val Glu Lys Arg Ser Gln His Ile Leu
230 235 240

Gln His Met Asp Phe Leu Tyr Tyr Leu Ser His Asp Gly Arg Arg
245 250 255

Phe His Arg Ala Cys Arg Leu Val His Asp Phe Thr Asp Ala Val
260 265 270

Ile Arg Glu Arg Arg Arg Thr Leu Pro Thr Gln Gly Ile Asp Asp
275 280 285

Phe Phe Lys Asp Lys Ala Lys Ser Lys Thr Leu Asp Phe Ile Asp
290 295 300

Val Leu Leu Leu Ser Lys Asp Glu Asp Gly Lys Ala Leu Ser Asp
305 310 315

Glu Asp Ile Arg Ala Glu Ala Asp Thr Phe Met Phe Gly Gly His
320 325 330

Asp Thr Thr Ala Ser Gly Leu Ser Trp Val Leu Tyr Asn Leu Ala
335 340 345

Arg His Pro Glu Tyr Gln Glu Arg Cys Arg Gln Glu Val Gln Glu
350 355 360

Leu Leu Lys Asp Arg Asp Pro Lys Glu Ile Glu Trp Asp Asp Leu
365 370 375

Ala Gln Leu Pro Phe Leu Thr Met Cys Val Lys Glu Ser Leu Arg
380 385 390

Leu His Pro Pro Ala Pro Phe Ile Ser Arg Cys Cys Thr Gln Asp
395 400 405

Ile Val Leu Pro Asp Gly Arg Val Ile Pro Lys Gly Ile Thr Cys
410 415 420

Leu Ile Asp Ile Ile Gly Val His His Asn Pro Thr Val Trp Pro
425 430 435

Asp Pro Glu Val Tyr Asp Pro Phe Arg Phe Asp Pro Glu Asn Ser
440 445 450

Lys Gly Arg Ser Pro Leu Ala Phe Ile Pro Phe Ser Ala Gly Pro
455 460 465

Arg Asn Cys Ile Gly Gln Ala Phe Ala Met Ala Glu Met Lys Val
470 475 480

Val Leu Ala Leu Met Leu Leu His Phe Arg Phe Leu Pro Asp His
485 490 495

Thr Glu Pro Arg Arg Lys Leu Glu Leu Ile Met Arg Ala Glu Gly
500 505 510

Gly Leu Trp Leu Arg Val Glu Pro Leu Asn Val Gly Leu Gln
515 520

<210> 265
<211> 584
<212> DNA
<213> Homo sapiens

<400> 265
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cagatattgc cagagatgct gggtgcagaa agaggggata ttctcaggaa 250

agcagactca agtaccaaca tttttaaccc aagaggaaat ttgagaaagt 300

ttcaggattt ctctggacaa gatcctaaca ttttactgag tcatcttttg 350

gccagaatct ggaaaccata caagaaacgt gagactcctg attgcttctg 400

gaaatactgt gtctgaagtg aaataagcat ctgttagtca gctcagaaac 450

acccatctta gaatatgaaa aataacacaa tgcttgattt gaaaacagtg 500

tggagaaaaa ctaggcaaac tacaccctgt tcattgttac ctggaaaata 550

aatcctctat gttttgcaca aaaaaaaaaa aaaa 584

<210> 266
<211> 124
<212> PRT
<213> Homo sapiens

<400> 266
Met Tyr Lys Leu Ala Ser Cys Cys Leu Leu Phe Thr Gly Phe Leu
1 5 10 15

Asn Pro Leu Leu Ser Leu Pro Leu Leu Asp Ser Arg Glu Ile Ser
20 25 30

Phe Gln Leu Ser Ala Pro His Glu Asp Ala Arg Leu Thr Pro Glu
35 40 45

Glu Leu Glu Arg Ala Ser Leu Leu Gln Ile Leu Pro Glu Met Leu
50 55 60

Gly Ala Glu Arg Gly Asp Ile Leu Arg Lys Ala Asp Ser Ser Thr
65 70 75

Asn Ile Phe Asn Pro Arg Gly Asn Leu Arg Lys Phe Gln Asp Phe
80 85 90

Ser Gly Gln Asp Pro Asn Ile Leu Leu Ser His Leu Leu Ala Arg
95 100 105

Ile Trp Lys Pro Tyr Lys Lys Arg Glu Thr Pro Asp Cys Phe Trp
110 115 120

Lys Tyr Cys Val

<210> 267
<211> 654
<212> DNA
<213> Homo sapiens

<400> 267
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cacctctggg atggggttgc tggtttaaaa caaacgccag tcatcctata 100

taaggacctg acagccacca ggcaccacct ccgccaggaa ctgcaggccc 150

acctgtctgc aacccagctg aggccatgcc ctccccaggg accgtctgca 200

gcctcctgct cctcggcatg ctctggctgg acttggccat ggcaggctcc 250

agcttcctga gccctgaaca ccagagagtc cagcagagaa aggagtcgaa 300

gaagccacca gccaagctgc agccccgagc tctagcaggc tggctccgcc 350

cggaagatgg aggtcaagca gaaggggcag aggatgaact ggaagtccgg 400

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<213> Homo sapiens

<400> 268
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Glu His Gln Arg Val Gln Gln Arg Lys Glu Ser Lys Lys Pro Pro
35 40 45

Ala Lys Leu Gln Pro Arg Ala Leu Ala Gly Trp Leu Arg Pro Glu
50 55 60

Asp Gly Gly Gln Ala Glu Gly Ala Glu Asp Glu Leu Glu Val Arg
65 70 75

Phe Asn Ala Pro Phe Asp Val Gly Ile Lys Leu Ser Gly Val Gln
80 85 90

Tyr Gln Gln His Ser Gln Ala Leu Gly Lys Phe Leu Gln Asp Ile
95 100 105

Leu Trp Glu Glu Ala Lys Glu Ala Pro Ala Asp Lys
110 115

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<212> DNA
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<211> 142
<212> PRT
<213> Homo sapiens

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			20					25						30	
Asp	Phe	Leu	Gly	Leu	Val	His	Leu	Gly	Gln	Leu	Leu	Ile	Phe	His	
			35					40						45	
Ile	Tyr	Leu	Ser	Met	Ser	Pro	Thr	Leu	Ser	Pro	Arg	Ser	Pro	Gln	
			50					55						60	
Gly	Trp	Val	Val	Arg	Ala	Ala	His	Leu	Thr	Pro	Leu	Leu	Glu	Tyr	
			65					70						75	
Val	Pro	Asn	Pro	Glu	Pro	Pro	Thr	Pro	Gly	Ala	Arg	Val	Phe	Val	
			80					85						90	
Pro	Arg	Val	Arg	Met	Cys	Ser	Gly	Ser	Ala	Ser	Pro	Arg	Ser	Glu	
			95					100						105	
Ile	Met	Asp	Lys	Lys	Gly	Lys	Ser	Gln	Glu	Glu	Ile	Lys	Ser	Met	
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Arg	Thr	Gln	Gln	Ala	Gln	Gln	Glu	Ala	Glu	Leu	Thr	Pro	Arg	Pro	
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<212> DNA
<213> Homo sapiens

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ctggggatga ccggttctcc ttccggagct tccggagtgg catgtggcta 350

tcctgtgagg aaactgtgga agaaccaggg gagaggtgcc gaagtttcat 400

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<211> 285
<212> PRT
<213> Homo sapiens

<400> 272

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Leu	Leu	Ser	Ala	Ile	Leu	Ser	Met	Leu	Ser	Leu	Ser	Phe	Ser	Thr	
				20				25						30	

Thr	Ser	Leu	Leu	Ser	Asn	Tyr	Trp	Phe	Val	Gly	Thr	Gln	Lys	Val	

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35 40 45

Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp
50 55 60

Met Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu
65 70 75

Val Val Gln Tyr Asn Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe
80 85 90

Arg Ser Phe Arg Ser Gly Met Trp Leu Ser Cys Glu Glu Thr Val
95 100 105

Glu Glu Pro Gly Glu Arg Cys Arg Ser Phe Ile Glu Leu Thr Pro
110 115 120

Pro Ala Lys Arg Gly Glu Lys Gly Leu Leu Glu Phe Ala Thr Leu
125 130 135

Gln Gly Pro Cys His Pro Thr Leu Arg Phe Gly Gly Lys Arg Leu
140 145 150

Met Glu Lys Ala Ser Leu Pro Ser Pro Pro Leu Gly Leu Cys Gly
155 160 165

Lys Asn Pro Met Val Ile Pro Gly Asn Ala Asp His Leu His Arg
170 175 180

Thr Ser Ile His Gln Leu Pro Pro Ala Thr Asn Arg Leu Ala Thr
185 190 195

His Trp Glu Pro Cys Leu Trp Ala Gln Thr Glu Arg Leu Cys Cys
200 205 210

Cys Phe Leu Cys Pro Val Arg Ser Pro Gly Asp Gly Gly Pro His
215 220 225

Asp Val Phe Thr Ser Leu Pro Ser Asp Cys Gln Leu Gly Ser Arg
230 235 240

Arg Leu Glu Thr Thr Cys Leu Glu Leu Trp Leu Gly Leu Leu His
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accaaccagg gtagtggcat ggagcaccgt aaccatctgt gcttctgtga 250

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<210> 274
<211> 86
<212> PRT
<213> Homo sapiens

<400> 274

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				20				25						30	
Leu	Leu	Trp	Thr	Leu	Pro	Ser	Pro	Leu	Val	Ala	Phe	Arg	Ala	Asn	
				35				40						45	
Arg	Thr	Thr	Tyr	Val	Met	Asp	Val	Ser	Thr	Asn	Gln	Gly	Ser	Gly	
				50				55						60	
Met	Glu	His	Arg	Asn	His	Leu	Cys	Phe	Cys	Asp	Leu	Tyr	Asp	Arg	
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<213> Homo sapiens

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Ile	Gly	Leu	Met	Phe	Leu	Met	Leu	Gly	Cys	Ala	Leu	Pro	Ile	Tyr	
			20					25						30	
Asn	Lys	Tyr	Trp	Pro	Leu	Phe	Val	Leu	Phe	Phe	Tyr	Ile	Leu	Ser	

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                65                  70                  75

Gly Ile Val Val Ser Ala Phe Gly Leu Pro Ile Val Phe Ala Arg
                80                  85                  90

Ala His Leu Ile Glu Trp Gly Ala Cys Ala Leu Val Leu Thr Gly
                95                 100                 105

Asn Thr Val Ile Phe Ala Thr Ile Leu Gly Phe Phe Leu Val Phe
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aacgggaatt tagctcacat catttcatgc ccctgtgcct ctagctctgg 2900

agattggtgg ggggaggtgg ggggaaacgg caggaataag ggaaagtggt 2950

agttttaact aaggttttgt aacacttgaa atcttttctt tctcaaatta 3000

attatcttta agcttcaaga aacttgctct gacccctcta agcaaactac 3050

taagcattta aaagagaatc taatttttaa aggtgtagca cctttttttt 3100

tattcttccc acagagggtg ctaatctcat tatgctgtgc tatctgaaaa 3150

gaacttaagg ccacaattca cgtctcgtcc tgggcattgt gatggattga 3200

ccctccattt gcagtacctt cccagctgat taaagttcag cagtggtatt 3250

gaggtttttc gaatatttat atagaaaaaa agtcttttca catgacaaat 3300

gacactctca caccagtctt agccctagta gtttttttagg ttggaccaga 3350

ggaagcaggt taaatgagac ctgtcctctg ctgcactcag aaaaaatagg 3400

cagtccctga tgctcagatc ttagccttga tattaatagt tgagaccacc 3450

tacccacaat gcagcctata ctcccaagac tacaaagtta ccatcgcaaa 3500

ggaaaggtta ttccagtaaa aggaaatagt tttctcaacc atttaaaaat 3550

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cttcaagaag gcagacattt ggtatgattt agcatcaaca acacatttat 3650

gagtatatgt aagtaatcag aggggcaaat gccacttgtt attcctccca 3700

agttttccaa gcaagtacac acagatctct ggtaggatta ggggccactt 3750

gtgtttccgg cttattttag tcgacttgtc agcaagtttg atgcctagtc 3800

tatctgacat ggcccagtag aacagggcat tgatggatca catgagatgg 3850

tagaaggaac atcatcacat acccctctca cagagaaaat tatcaaagaa 3900

ccagaaatta tatctgtttt ggagcaagag tgtcataatg tttcagggta 3950

gtcaaaataa acataaatta tctcctctag atgagtggcg atgttggctg 4000

atttgggtct gccattgaca gaatgtcaaa taaaaaggaa ttagctagaa 4050

tatgaccatt aaatgtgctt ctgaaatata ttttgagata ggtttagaat 4100

gtca 4104

<210> 278
<211> 522
<212> PRT
<213> Homo sapiens

<400> 278

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 Met Asp Phe Leu Leu Leu Gly Leu Cys Leu Tyr Trp Leu Leu Arg
   1               5                  10                  15

 Arg Pro Ser Gly Val Val Leu Cys Leu Leu Gly Ala Cys Phe Gln
                20                  25                  30

 Met Leu Pro Ala Ala Pro Ser Gly Cys Pro Gln Leu Cys Arg Cys
                35                  40                  45

 Glu Gly Arg Leu Leu Tyr Cys Glu Ala Leu Asn Leu Thr Glu Ala
                50                  55                  60

 Pro His Asn Leu Ser Gly Leu Leu Gly Leu Ser Leu Arg Tyr Asn
                65                  70                  75

 Ser Leu Ser Glu Leu Arg Ala Gly Gln Phe Thr Gly Leu Met Gln
                80                  85                  90

 Leu Thr Trp Leu Tyr Leu Asp His Asn His Ile Cys Ser Val Gln
                95                 100                 105

 Gly Asp Ala Phe Gln Lys Leu Arg Arg Val Lys Glu Leu Thr Leu
               110                 115                 120

 Ser Ser Asn Gln Ile Thr Gln Leu Pro Asn Thr Thr Phe Arg Pro
               125                 130                 135

 Met Pro Asn Leu Arg Ser Val Asp Leu Ser Tyr Asn Lys Leu Gln
               140                 145                 150

 Ala Leu Ala Pro Asp Leu Phe His Gly Leu Arg Lys Leu Thr Thr
               155                 160                 165

 Leu His Met Arg Ala Asn Ala Ile Gln Phe Val Pro Val Arg Ile
               170                 175                 180

 Phe Gln Asp Cys Arg Ser Leu Lys Phe Leu Asp Ile Gly Tyr Asn
               185                 190                 195

 Gln Leu Lys Ser Leu Ala Arg Asn Ser Phe Ala Gly Leu Phe Lys
               200                 205                 210

 Leu Thr Glu Leu His Leu Glu His Asn Asp Leu Val Lys Val Asn
               215                 220                 225

 Phe Ala His Phe Pro Arg Leu Ile Ser Leu His Ser Leu Cys Leu
               230                 235                 240

 Arg Arg Asn Lys Val Ala Ile Val Val Ser Ser Leu Asp Trp Val
               245                 250                 255

 Trp Asn Leu Glu Lys Met Asp Leu Ser Gly Asn Glu Ile Glu Tyr
               260                 265                 270

 Met Glu Pro His Val Phe Glu Thr Val Pro His Leu Gln Ser Leu
               275                 280                 285
```

Gln Leu Asp Ser Asn Arg Leu Thr Tyr Ile Glu Pro Arg Ile Leu
290 295 300

Asn Ser Trp Lys Ser Leu Thr Ser Ile Thr Leu Ala Gly Asn Leu
305 310 315

Trp Asp Cys Gly Arg Asn Val Cys Ala Leu Ala Ser Trp Leu Ser
320 325 330

Asn Phe Gln Gly Arg Tyr Asp Gly Asn Leu Gln Cys Ala Ser Pro
335 340 345

Glu Tyr Ala Gln Gly Glu Asp Val Leu Asp Ala Val Tyr Ala Phe
350 355 360

His Leu Cys Glu Asp Gly Ala Glu Pro Thr Ser Gly His Leu Leu
365 370 375

Ser Ala Val Thr Asn Arg Ser Asp Leu Gly Pro Pro Ala Ser Ser
380 385 390

Ala Thr Thr Leu Ala Asp Gly Gly Glu Gly Gln His Asp Gly Thr
395 400 405

Phe Glu Pro Ala Thr Val Ala Leu Pro Gly Gly Glu His Ala Glu
410 415 420

Asn Ala Val Gln Ile His Lys Val Val Thr Gly Thr Met Ala Leu
425 430 435

Ile Phe Ser Phe Leu Ile Val Val Leu Val Leu Tyr Val Ser Trp
440 445 450

Lys Cys Phe Pro Ala Ser Leu Arg Gln Leu Arg Gln Cys Phe Val
455 460 465

Thr Gln Arg Arg Lys Gln Lys Gln Lys Gln Thr Met His Gln Met
470 475 480

Ala Ala Met Ser Ala Gln Glu Tyr Tyr Val Asp Tyr Lys Pro Asn
485 490 495

His Ile Glu Gly Ala Leu Val Ile Ile Asn Glu Tyr Gly Ser Cys
500 505 510

Thr Cys His Gln Gln Pro Ala Arg Glu Cys Glu Val
515 520

<210> 279
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 279
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<210> 280
<211> 709
<212> DNA
<213> Homo sapiens

<400> 280
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ctgcagctct gcgcactgac ccaggcggtc tccaaactct gggtccccaa 100

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ccggcggcgc cgttgagttc ccggcggaca agatggtgtc agtcctggtg 200

caagaaggtc acgccgtctc agacatgctc ctgccgctgg atggggaact 250

cgtcctggct tcaggagccg gattcggcgt ctcagacgtg ggctcgcacc 300

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ggacctggct gttttcctgg cgtcccgcgc gggccgccta cgcttccacg 600

ggccgggcgc gctgagcgtg ggccccgagg actgcgcgga cccgtcgggc 650

tgcgtctgcg gcaacgcgga ggcgcagccg tggatctgcg cggccctgct 700

ccagcccct 709

<210> 281
<211> 229
<212> PRT
<213> Homo sapiens

<400> 281
Met Gly Val Leu Gly Arg Val Leu Leu Trp Leu Gln Leu Cys Ala
1 5 10 15

Leu Thr Gln Ala Val Ser Lys Leu Trp Val Pro Asn Thr Asp Phe
20 25 30

Asp Val Ala Ala Asn Trp Ser Gln Asn Arg Thr Pro Cys Ala Gly
35 40 45

Gly Ala Val Glu Phe Pro Ala Asp Lys Met Val Ser Val Leu Val
50 55 60

Gln Glu Gly His Ala Val Ser Asp Met Leu Leu Pro Leu Asp Gly
65 70 75

Glu Leu Val Leu Ala Ser Gly Ala Gly Phe Gly Val Ser Asp Val
80 85 90

Gly Ser His Leu Asp Cys Gly Ala Gly Glu Pro Ala Val Phe Arg
95 100 105

Asp Ser Asp Arg Phe Ser Trp His Asp Pro His Leu Trp Arg Ser
110 115 120

Gly Asp Glu Ala Pro Gly Leu Phe Phe Val Asp Ala Glu Arg Val
125 130 135

Pro Cys Arg His Asp Asp Val Phe Phe Pro Pro Ser Ala Ser Phe
140 145 150

Arg Val Gly Leu Gly Pro Gly Ala Ser Pro Val Arg Val Arg Ser
155 160 165

Ile Ser Ala Leu Gly Arg Thr Phe Thr Arg Asp Glu Asp Leu Ala
170 175 180

Val Phe Leu Ala Ser Arg Ala Gly Arg Leu Arg Phe His Gly Pro
185 190 195

Gly Ala Leu Ser Val Gly Pro Glu Asp Cys Ala Asp Pro Ser Gly
200 205 210

Cys Val Cys Gly Asn Ala Glu Ala Gln Pro Trp Ile Cys Ala Ala
215 220 225

Leu Leu Gln Pro

<210> 282
<211> 644
<212> DNA
<213> Homo sapiens

<400> 282
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gaagcgaatg tttgagccta ctcgtttgat tgcaactatc atggtgctgt 100

tgtgttttgc acttaccctg tgttctgcct tttggtggca taacaaggga 150

cttgcactta tcttctgcat tttgcagtct ttggcattga cgtggtacag 200

cctttccttc ataccatttg caagggatgc tgtgaagaag tgttttgccg 250

tgtgtcttgc ataattcatg gccagtttta tgaagctttg gaaggcacta 300

tggacagaag ctggtggaca gttttgtaac tatcttcgaa acctctgtct 350

tacagacatg tgccttttat cttgcagcaa tgtgttgctt gtgattcgaa 400

catttgaggg ttacttttgg aagcaacaat acattctcga acctgaatgt 450

cagtagcaca ggatgagaag tgggttctgt atcttgtgga gtggaatctt 500

cctcatgtac ctgtttcctc tctggatgtt gtcccactga attcccatga 550

atacaaacct attcagcaac agcaaaaaaa aaaaaaaaaa aaaaaaaaaa 600

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 644

<210> 283
<211> 77
<212> PRT
<213> Homo sapiens

<400> 283
Met Gly Pro Val Lys Gln Leu Lys Arg Met Phe Glu Pro Thr Arg
1 5 10 15

Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe Ala Leu Thr Leu

20 25 30

Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala Leu Ile Phe
35 40 45

Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu Ser Phe
50 55 60

Ile Pro Phe Ala Arg Asp Ala Val Lys Lys Cys Phe Ala Val Cys
65 70 75

Leu Ala

<210> 284
<211> 2623
<212> DNA
<213> Homo sapiens

<400> 284
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ctcccgccgt tacccgcggc gcgcccgagg gagtctcctc cagaccctcc 100

ctcccgttgc tccaaactaa tacggactga acggatcgct gcgagggtgg 150

gagagaaaat taggggggaga aaggacagag agagcaacta ccatccatag 200

ccagatagat tatcttacac tgaactgatc aagtactttg aaaatgactt 250

cgaaatttat cttggtgtcc ttcatacttg ctgcactgag tctttcaacc 300

acctttttctc tccaactaga ccagcaaaag gttctactag tttcttttga 350

tggattccgt tgggattact tatataaagt tccaacgccc cattttcatt 400

atattatgaa atatggtgtt cacgtgaagc aagttactaa tgtttttatt 450

acaaaaacct accctaacca ttatactttg gtaactggcc tctttgcaga 500

gaatcatggg attgttgcaa atgatatgtt tgatcctatt cggaacaaat 550

ctttctcctt ggatcacatg aatatttatg attccaagtt ttgggaagaa 600

gcgacaccaa tatggatcac aaaccagagg gcaggacata ctagtggtgc 650

agccatgtgg cccggaacag atgtaaaaat acataagcgc tttcctactc 700

attacatgcc ttacaatgag tcagtttcat ttgaagatag agttgccaaa 750

attgttgaat ggtttacgtc aaaagagccc ataaatcttg gtcttctcta 800

ttgggaagac cctgatgaca tgggccacca tttgggacct gacagtccgc 850

tcatggggcc tgtcatttca gatattgaca agaagttagg atatctcata 900

caaatgctga aaaaggcaaa gttgtggaac actctgaacc taatcatcac 950

aagtgatcat ggaatgacgc agtgctctga ggaaaggtta atagaacttg 1000

accagtacct ggataaagac cactataccc tgattgatca atctccagta 1050

gcagccatct tgccaaaaga aggtaaattt gatgaagtct atgaagcact 1100

aactcacgct catcctaatc ttactgttta caaaaaagaa gacgttccag 1150

aaaggtggca ttacaaatac aacagtcgaa ttcaaccaat catagcagtg 1200

gctgatgaag ggtggcacat tttacagaat aagtcagatg actttctgtt 1250

aggcaaccac ggttacgata atgcgttagc agatatgcat ccaatatttt 1300

tagcccatgg tcctgccttc agaaagaatt tctcaaaaga agccatgaac 1350

tccacagatt tgtacccact actatgccac ctcctcaata tcactgccat 1400

gccacacaat ggatcattct ggaatgtcca ggatctgctc aattcagcaa 1450

tgccaagggt ggtcccttat acacagagta ctatactcct ccctggtagt 1500

gttaaaccag cagaatatga ccaagagggg tcataccctt atttcatagg 1550

ggtctctctt ggcagcatta tagtgattgt atttttttgta attttcatta 1600

agcatttaat tcacagtcaa atacctgcct tacaagatat gcatgctgaa 1650

atagctcaac cattattaca agcctaatgt tactttgaag tggatttgca 1700

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ctgggaaacc agttccaaac atctgcagaa accattaagc agttacatat 1800

ttaggtatac acacacacac acacacacac atacacacac acggaccaaa 1850

atacttacac ctgcaaagga ataaagatgt gagagtatgt ctccattgtt 1900

cactgtagca tagggataga taagatcctg ctttatttgg acttggcgca 1950

gataatgtat atatttagca actttgcact atgtaaagta ccttatatat 2000

tgcactttaa atttctctcc tgatgggtac tttaatttga aatgcacttt 2050

atggacagtt atgtcttata acttgattga aaatgacaac tttttgcacc 2100

catgtcacag aatacttgtt acgcattgtt caaactgaag gaaatttcta 2150

ataatcccga ataatgaaca tagaaatcta tctccataaa ttgagagaag 2200

aagaaggtga taagtgttga aaattaaatg tgataacctt tgaaccttga 2250

attttggaga tgtattccca acagcagaat gcaactgtgg gcatttcttg 2300

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aagacaccat gaatatactt ttcttctata tagttcagca atggcctgaa 2500

tagaagcaac caggcaccat ctcagcaatg ttttctcttg tttgtaatta 2550

tttgctcctt tgaaaattaa atcactatta attacattaa aaatcaaatt 2600

ggataaaaaa aaaaaaaaaa aaa 2623

<210> 285

<211> 477
<212> PRT
<213> Homo sapiens

<400> 285

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Met Thr Ser Lys Phe Ile Leu Val Ser Phe Ile Leu Ala Ala Leu
  1               5                  10                  15

Ser Leu Ser Thr Thr Phe Ser Leu Gln Leu Asp Gln Gln Lys Val
             20                  25                  30

Leu Leu Val Ser Phe Asp Gly Phe Arg Trp Asp Tyr Leu Tyr Lys
             35                  40                  45

Val Pro Thr Pro His Phe His Tyr Ile Met Lys Tyr Gly Val His
             50                  55                  60

Val Lys Gln Val Thr Asn Val Phe Ile Thr Lys Thr Tyr Pro Asn
             65                  70                  75

His Tyr Thr Leu Val Thr Gly Leu Phe Ala Glu Asn His Gly Ile
             80                  85                  90

Val Ala Asn Asp Met Phe Asp Pro Ile Arg Asn Lys Ser Phe Ser
             95                 100                 105

Leu Asp His Met Asn Ile Tyr Asp Ser Lys Phe Trp Glu Glu Ala
            110                 115                 120

Thr Pro Ile Trp Ile Thr Asn Gln Arg Ala Gly His Thr Ser Gly
            125                 130                 135

Ala Ala Met Trp Pro Gly Thr Asp Val Lys Ile His Lys Arg Phe
            140                 145                 150

Pro Thr His Tyr Met Pro Tyr Asn Glu Ser Val Ser Phe Glu Asp
            155                 160                 165

Arg Val Ala Lys Ile Val Glu Trp Phe Thr Ser Lys Glu Pro Ile
            170                 175                 180

Asn Leu Gly Leu Leu Tyr Trp Glu Asp Pro Asp Asp Met Gly His
            185                 190                 195

His Leu Gly Pro Asp Ser Pro Leu Met Gly Pro Val Ile Ser Asp
            200                 205                 210

Ile Asp Lys Lys Leu Gly Tyr Leu Ile Gln Met Leu Lys Lys Ala
            215                 220                 225

Lys Leu Trp Asn Thr Leu Asn Leu Ile Ile Thr Ser Asp His Gly
            230                 235                 240

Met Thr Gln Cys Ser Glu Glu Arg Leu Ile Glu Leu Asp Gln Tyr
            245                 250                 255

Leu Asp Lys Asp His Tyr Thr Leu Ile Asp Gln Ser Pro Val Ala
            260                 265                 270

Ala Ile Leu Pro Lys Glu Gly Lys Phe Asp Glu Val Tyr Glu Ala
            275                 280                 285

Leu Thr His Ala His Pro Asn Leu Thr Val Tyr Lys Lys Glu Asp
```

290 295 300

Val Pro Glu Arg Trp His Tyr Lys Tyr Asn Ser Arg Ile Gln Pro
305 310 315

Ile Ile Ala Val Ala Asp Glu Gly Trp His Ile Leu Gln Asn Lys
320 325 330

Ser Asp Asp Phe Leu Leu Gly Asn His Gly Tyr Asp Asn Ala Leu
335 340 345

Ala Asp Met His Pro Ile Phe Leu Ala His Gly Pro Ala Phe Arg
350 355 360

Lys Asn Phe Ser Lys Glu Ala Met Asn Ser Thr Asp Leu Tyr Pro
365 370 375

Leu Leu Cys His Leu Leu Asn Ile Thr Ala Met Pro His Asn Gly
380 385 390

Ser Phe Trp Asn Val Gln Asp Leu Leu Asn Ser Ala Met Pro Arg
395 400 405

Val Val Pro Tyr Thr Gln Ser Thr Ile Leu Leu Pro Gly Ser Val
410 415 420

Lys Pro Ala Glu Tyr Asp Gln Glu Gly Ser Tyr Pro Tyr Phe Ile
425 430 435

Gly Val Ser Leu Gly Ser Ile Ile Val Ile Val Phe Phe Val Ile
440 445 450

Phe Ile Lys His Leu Ile His Ser Gln Ile Pro Ala Leu Gln Asp
455 460 465

Met His Ala Glu Ile Ala Gln Pro Leu Leu Gln Ala
470 475

<210> 286
<211> 1337
<212> DNA
<213> Homo sapiens

<400> 286
ggatttttgt gatccgcgat tcgctcccac gggcgggacc tttgtaactg 50

cgggaggccc aggacaggcc caccctgcgg ggcgggaggc agccggggtg 100

agggaggtga agaaaccaag acgcagagag gccaagcccc ttgccttggg 150

tcacacagcc aaaggaggca gagccagaac tcacaaccag atccagaggc 200

aacagggaca tggccacctg ggacgaaaag gcagtcaccc gcagggccaa 250

ggtggctccc gctgagagga tgagcaagtt cttaaggcac ttcacggtcg 300

tgggagacga ctaccatgcc tggaacatca actacaagaa atgggagaat 350

gaagaggagg aggaggagga ggagcagcca ccacccacac cagtctcagg 400

cgaggaaggc agagctgcag cccctgacgt tgcccctgcc cctggccccg 450

cacccagggc ccccttgac ttcaggggca tgttgaggaa actgttcagc 500

tcccacaggt ttcaggtcat catcatctgc ttggtggttc tggatgccct 550

cctggtgctt gctgagctca tcctggacct gaagatcatc cagcccgaca 600

agaataacta tgctgccatg gtattccact acatgagcat caccatcttg 650

gtctttttta tgatggagat catctttaaa ttatttgtct tccgcctgag 700

ttctttcacc acaagtttga gatcctggat gcccgtcgtg gtggtggtct 750

cattcatcct ggacattgtc ctcctgttcc aggagcacca gtttgaggct 800

ctgggcctgc tgattctgct ccggctgtgg cgggtggccc ggatcatcaa 850

tgggattatc atctcagtta agacacgttc agaacggcaa ctcttaaggt 900

taaaacagat gaatgtacaa ttggccgcca agattcaaca ccttgagttc 950

agctgctctg agaagcccct ggactgatga gtttgctgta tcaacctgta 1000

aggagaagct ctctccggat ggctatggga atgaaagaat ccgacttcta 1050

ctctcacaca gccaccgtga aagtcctgga gtaaaatgtg ctgtgtacag 1100

aagagagaga aggaagcagg ctggcatgtt cactgggctg gtgttacgac 1150

agagaacctg acagtcactg gccagttatc acttcagatt acaaatcaca 1200

cagagcatct gcctgtttic aatcacaaga gaacaaaacc aaaatctata 1250

aagatattct gaaaatatga cagaatttga caaataaaag cataaacgtg 1300

taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1337

<210> 287
<211> 255
<212> PRT
<213> Homo sapiens

<400> 287

Met	Ala	Thr	Trp	Asp	Glu	Lys	Ala	Val	Thr	Arg	Arg	Ala	Lys	Val	
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Ala	Pro	Ala	Glu	Arg	Met	Ser	Lys	Phe	Leu	Arg	His	Phe	Thr	Val	
				20				25						30	
Val	Gly	Asp	Asp	Tyr	His	Ala	Trp	Asn	Ile	Asn	Tyr	Lys	Lys	Trp	
				35				40						45	
Glu	Asn	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gln	Pro	Pro	Pro	Thr	
				50				55						60	
Pro	Val	Ser	Gly	Glu	Glu	Gly	Arg	Ala	Ala	Ala	Pro	Asp	Val	Ala	
				65				70						75	
Pro	Ala	Pro	Gly	Pro	Ala	Pro	Arg	Ala	Pro	Leu	Asp	Phe	Arg	Gly	
				80				85						90	
Met	Leu	Arg	Lys	Leu	Phe	Ser	Ser	His	Arg	Phe	Gln	Val	Ile	Ile	
				95				100						105	
Ile	Cys	Leu	Val	Val	Leu	Asp	Ala	Leu	Leu	Val	Leu	Ala	Glu	Leu	
				110				115						120	

Ile Leu Asp Leu Lys Ile Ile Gln Pro Asp Lys Asn Asn Tyr Ala
125 130 135

Ala Met Val Phe His Tyr Met Ser Ile Thr Ile Leu Val Phe Phe
140 145 150

Met Met Glu Ile Ile Phe Lys Leu Phe Val Phe Arg Leu Ser Ser
155 160 165

Phe Thr Thr Ser Leu Arg Ser Trp Met Pro Val Val Val Val Val
170 175 180

Ser Phe Ile Leu Asp Ile Val Leu Leu Phe Gln Glu His Gln Phe
185 190 195

Glu Ala Leu Gly Leu Leu Ile Leu Leu Arg Leu Trp Arg Val Ala
200 205 210

Arg Ile Ile Asn Gly Ile Ile Ile Ser Val Lys Thr Arg Ser Glu
215 220 225

Arg Gln Leu Leu Arg Leu Lys Gln Met Asn Val Gln Leu Ala Ala
230 235 240

Lys Ile Gln His Leu Glu Phe Ser Cys Ser Glu Lys Pro Leu Asp
245 250 255

<210> 288
<211> 3334
<212> DNA
<213> Homo sapiens

<400> 288
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ggccgccaac atgctctgtc tgtgcctgta cgtgccggtc atcggggaag 100

cccagaccga gttccagtac tttgagtcga aggggctccc tgccgagctg 150

aagtccattt tcaagctcag tgtcttcatc ccctcccagg aattctccac 200

ctaccgccag tggaagcaga aaattgtaca agctggagat aaggaccttg 250

atgggcagct agactttgaa gaatttgtcc attatctcca agatcatgag 300

aagaagctga ggctggtgtt taagattttg gacaaaaaga atgatggacg 350

cattgacgcg caggagatca tgcagtccct gcgggacttg ggagtcaaga 400

tatctgaaca gcaggcagaa aaaattctca agagcatgga taaaaacggc 450

acgatgacca tcgactggaa cgagtggaga gactaccacc tcctccaccc 500

cgtggaaaac atccccgaga tcatcctcta ctggaagcat tccacgatct 550

ttgatgtggg tgagaatcta acggtcccgg atgagttcac agtggaggag 600

aggcagacgg ggatgtggtg gagacacctg gtggcaggag gtggggcagg 650

ggccgtatcc agaacctgca cggcccccct ggacaggctc aaggtgctca 700

tgcaggtcca tgcctcccgc agcaacaaca tgggcatcgt tggtggcttc 750

actcagatga ttcgagaagg aggggccagg tcactctggc ggggcaatgg 800

catcaacgtc ctcaaaattg cccccgaatc agccatcaaa ttcatggcct 850

atgagcagat caagcgcctt gttggtagtg accaggagac tctgaggatt 900

cacgagaggc ttgtggcagg gtccttggca ggggccatcg cccagagcag 950

catctaccca atggaggtcc tgaagacccg gatggcgctg cggaagacag 1000

gccagtactc aggaatgctg gactgcgcca ggaggatcct ggccagagag 1050

ggggtggccg ccttctacaa aggctatgtc cccaacatgc tgggcatcat 1100

cccctatgcc ggcatcgacc ttgcagtcta cgagacgctc aagaatgcct 1150

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ctggcctgtg gcaccatgtc cagtacctgt ggccagctgg ccagctaccc 1250

cctggcccta gtcaggaccc ggatgcaggc gcaagcctct attgagggcg 1300

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ggggccttcg ggctgtacag ggggctggcc cccaacttca tgaaggtcat 1400

cccagctgtg agcatcagct acgtggtcta cgagaacctg aagatcaccc 1450

tgggcgtgca gtcgcggtga cgggggggagg gccgcccggc agtggactcg 1500

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tgccaacact aagctgtctc gagccaagct gtgaaaaccc tagacgcacc 1600

cgcagggagg gtggggagag ctggcaggcc cagggcttgt cctgctgacc 1650

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<210> 289
<211> 469
<212> PRT
<213> Homo sapiens

<400> 289

Met	Leu	Cys	Leu	Cys	Leu	Tyr	Val	Pro	Val	Ile	Gly	Glu	Ala	Gln	
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Thr	Glu	Phe	Gln	Tyr	Phe	Glu	Ser	Lys	Gly	Leu	Pro	Ala	Glu	Leu	
				20				25						30	
Lys	Ser	Ile	Phe	Lys	Leu	Ser	Val	Phe	Ile	Pro	Ser	Gln	Glu	Phe	
				35				40						45	
Ser	Thr	Tyr	Arg	Gln	Trp	Lys	Gln	Lys	Ile	Val	Gln	Ala	Gly	Asp	
				50				55						60	
Lys	Asp	Leu	Asp	Gly	Gln	Leu	Asp	Phe	Glu	Glu	Phe	Val	His	Tyr	
				65				70						75	
Leu	Gln	Asp	His	Glu	Lys	Lys	Leu	Arg	Leu	Val	Phe	Lys	Ile	Leu	
				80				85						90	

Asp Lys Lys Asn Asp Gly Arg Ile Asp Ala Gln Glu Ile Met Gln
95 100 105

Ser Leu Arg Asp Leu Gly Val Lys Ile Ser Glu Gln Gln Ala Glu
110 115 120

Lys Ile Leu Lys Ser Met Asp Lys Asn Gly Thr Met Thr Ile Asp
125 130 135

Trp Asn Glu Trp Arg Asp Tyr His Leu Leu His Pro Val Glu Asn
140 145 150

Ile Pro Glu Ile Ile Leu Tyr Trp Lys His Ser Thr Ile Phe Asp
155 160 165

Val Gly Glu Asn Leu Thr Val Pro Asp Glu Phe Thr Val Glu Glu
170 175 180

Arg Gln Thr Gly Met Trp Trp Arg His Leu Val Ala Gly Gly Gly
185 190 195

Ala Gly Ala Val Ser Arg Thr Cys Thr Ala Pro Leu Asp Arg Leu
200 205 210

Lys Val Leu Met Gln Val His Ala Ser Arg Ser Asn Asn Met Gly
215 220 225

Ile Val Gly Gly Phe Thr Gln Met Ile Arg Glu Gly Gly Ala Arg
230 235 240

Ser Leu Trp Arg Gly Asn Gly Ile Asn Val Leu Lys Ile Ala Pro
245 250 255

Glu Ser Ala Ile Lys Phe Met Ala Tyr Glu Gln Ile Lys Arg Leu
260 265 270

Val Gly Ser Asp Gln Glu Thr Leu Arg Ile His Glu Arg Leu Val
275 280 285

Ala Gly Ser Leu Ala Gly Ala Ile Ala Gln Ser Ser Ile Tyr Pro
290 295 300

Met Glu Val Leu Lys Thr Arg Met Ala Leu Arg Lys Thr Gly Gln
305 310 315

Tyr Ser Gly Met Leu Asp Cys Ala Arg Arg Ile Leu Ala Arg Glu
320 325 330

Gly Val Ala Ala Phe Tyr Lys Gly Tyr Val Pro Asn Met Leu Gly
335 340 345

Ile Ile Pro Tyr Ala Gly Ile Asp Leu Ala Val Tyr Glu Thr Leu
350 355 360

Lys Asn Ala Trp Leu Gln His Tyr Ala Val Asn Ser Ala Asp Pro
365 370 375

Gly Val Phe Val Leu Leu Ala Cys Gly Thr Met Ser Ser Thr Cys
380 385 390

Gly Gln Leu Ala Ser Tyr Pro Leu Ala Leu Val Arg Thr Arg Met
395 400 405

Gln Ala Gln Ala Ser Ile Glu Gly Ala Pro Glu Val Thr Met Ser
410 415 420

Ser Leu Phe Lys His Ile Leu Arg Thr Glu Gly Ala Phe Gly Leu
425 430 435

Tyr Arg Gly Leu Ala Pro Asn Phe Met Lys Val Ile Pro Ala Val
440 445 450

Ser Ile Ser Tyr Val Val Tyr Glu Asn Leu Lys Ile Thr Leu Gly
455 460 465

Val Gln Ser Arg

<210> 290
<211> 1658
<212> DNA
<213> Homo sapiens

<400> 290
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atttcaggga gacactccat cacagtcact actgtcgcct cagctgggaa 200

cattggggag gatggaatcc tgagctgcac ttttgaacct gacatcaaac 250

tttctgatat cgtgatacaa tggctgaagg aaggtgtttt aggcttggtc 300

catgagttca aagaaggcaa agatgagctg tcggagcagg atgaaatgtt 350

cagaggccgg acagcagtgt ttgctgatca agtgatagtt ggcaatgcct 400

ctttgcggct gaaaaacgtg caactcacag atgctggcac ctacaaatgt 450

tatatcatca cttctaaagg caaggggaat gctaaccttg agtataaaac 500

tggagccttc agcatgccgg aagtgaatgt ggactataat gccagctcag 550

agaccttgcg gtgtgaggct ccccgatggt tcccccagcc cacagtggtc 600

tgggcatccc aagttgacca gggagccaac ttctcggaag tctccaatac 650

cagctttgag ctgaactctg agaatgtgac catgaaggtt gtgtctgtgc 700

tctacaatgt tacgatcaac aacacatact cctgtatgat tgaaaatgac 750

attgccaaag caacagggga tatcaaagtg acagaatcgg agatcaaaag 800

gcggagtcac ctacagctgc taaactcaaa ggcttctctg tgtgtctctt 850

ctttctttgc catcagctgg gcacttctgc ctctcagccc ttacctgatg 900

ctaaaataat gtgccttggc cacaaaaaag catgcaaagt cattgttaca 950

acagggatct acagaactat ttcaccacca gatatgacct agttttatat 1000

ttctgggagg aaatgaattc atatctagaa gtctggagtg agcaaacaag 1050

agcaagaaac aaaaagaagc caaaagcaga aggctccaat atgaacaaga 1100

taaatctatc ttcaaagaca tattagaagt tgggaaaata attcatgtga 1150

actagacaag tgtgttaaga gtgataagta aaatgcacgt ggagacaagt 1200

gcatccccag atctcaggga cctccccctg cctgtcacct ggggagtgag 1250

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tgtaatgttg ctctgaggaa gcccctggaa agtctatccc aacatatcca 1350

catcttatat tccacaaatt aagctgtagt atgtacccta agacgctgct 1400

aattgactgc cacttcgcaa ctcaggggcg gctgcatttt agtaatgggt 1450

caaatgattc actttttatg atgcttccaa aggtgccttg gcttctcttc 1500

ccaactgaca aatgccaaag ttgagaaaaa tgatcataat tttagcataa 1550

acagagcagt cggggacacc gattttataa ataaactgag caccttcttt 1600

ttaaacaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650

aaaaaaaa 1658

<210> 291
<211> 282
<212> PRT
<213> Homo sapiens

<400> 291

Met	Ala	Ser	Leu	Gly	Gln	Ile	Leu	Phe	Trp	Ser	Ile	Ile	Ser	Ile	
1				5				10						15	
Ile	Ile	Ile	Leu	Ala	Gly	Ala	Ile	Ala	Leu	Ile	Ile	Gly	Phe	Gly	
				20				25						30	
Ile	Ser	Gly	Arg	His	Ser	Ile	Thr	Val	Thr	Thr	Val	Ala	Ser	Ala	
				35				40						45	
Gly	Asn	Ile	Gly	Glu	Asp	Gly	Ile	Leu	Ser	Cys	Thr	Phe	Glu	Pro	
				50				55						60	
Asp	Ile	Lys	Leu	Ser	Asp	Ile	Val	Ile	Gln	Trp	Leu	Lys	Glu	Gly	
				65				70						75	
Val	Leu	Gly	Leu	Val	His	Glu	Phe	Lys	Glu	Gly	Lys	Asp	Glu	Leu	
				80				85						90	
Ser	Glu	Gln	Asp	Glu	Met	Phe	Arg	Gly	Arg	Thr	Ala	Val	Phe	Ala	
				95				100						105	
Asp	Gln	Val	Ile	Val	Gly	Asn	Ala	Ser	Leu	Arg	Leu	Lys	Asn	Val	
				110				115						120	
Gln	Leu	Thr	Asp	Ala	Gly	Thr	Tyr	Lys	Cys	Tyr	Ile	Ile	Thr	Ser	
				125				130						135	
Lys	Gly	Lys	Gly	Asn	Ala	Asn	Leu	Glu	Tyr	Lys	Thr	Gly	Ala	Phe	
				140				145						150	
Ser	Met	Pro	Glu	Val	Asn	Val	Asp	Tyr	Asn	Ala	Ser	Ser	Glu	Thr	

155 160 165

Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln Pro Thr Val Val
170 175 180

Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser Glu Val Ser
185 190 195

Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met Lys Val
200 205 210

Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser Cys
215 220 225

Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val
230 235 240

Thr Glu Ser Glu Ile Lys Arg Arg Ser His Leu Gln Leu Leu Asn
245 250 255

Ser Lys Ala Ser Leu Cys Val Ser Ser Phe Phe Ala Ile Ser Trp
260 265 270

Ala Leu Leu Pro Leu Ser Pro Tyr Leu Met Leu Lys
275 280

<210> 292
<211> 1484
<212> DNA
<213> Homo sapiens

<400> 292
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tgaagcgggc ctccgccggc ctgcagcggg ttcatgagcc gacctgggcc 150

cagcagttgc tacaggagat gaagaccctc ttcttgaata ctgagtacct 200

gatgcccttt ctcctcaacc agtgtggatc ccttctctat tacctcacct 250

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atcatcttca cactgattgt tgggaaggcc cttggagaag atattggtgg 350

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gacatacctg tgttagttcc ttcccagaac ccatctcccc agagtgggtg 450

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ccttgtggcc atcagagttc ccttcccctg gacagtctgg agaaagacag 550

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cagccccacc tgactccagc acacctggcg agtagtagct gtcaataaat 1400

ctatgtaaac agacaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1450

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1484

<210> 293
<211> 180
<212> PRT
<213> Homo sapiens

<400> 293

Met	Ala	Ala	Ser	Leu	Gly	Gln	Val	Leu	Ala	Leu	Val	Leu	Val	Ala	
1				5				10						15	
Ala	Leu	Trp	Gly	Gly	Thr	Gln	Pro	Leu	Leu	Lys	Arg	Ala	Ser	Ala	
				20				25						30	
Gly	Leu	Gln	Arg	Val	His	Glu	Pro	Thr	Trp	Ala	Gln	Gln	Leu	Leu	
				35				40						45	
Gln	Glu	Met	Lys	Thr	Leu	Phe	Leu	Asn	Thr	Glu	Tyr	Leu	Met	Pro	
				50				55						60	
Phe	Leu	Leu	Asn	Gln	Cys	Gly	Ser	Leu	Leu	Tyr	Tyr	Leu	Thr	Leu	
				65				70						75	
Ala	Ser	Thr	Asp	Leu	Thr	Leu	Ala	Val	Pro	Ile	Cys	Asn	Ser	Leu	
				80				85						90	
Ala	Ile	Ile	Phe	Thr	Leu	Ile	Val	Gly	Lys	Ala	Leu	Gly	Glu	Asp	
				95				100						105	
Ile	Gly	Gly	Lys	Arg	Lys	Leu	Asp	Tyr	Cys	Glu	Cys	Gly	Thr	Gln	
				110				115						120	
Leu	Cys	Gly	Ser	Arg	His	Thr	Cys	Val	Ser	Ser	Phe	Pro	Glu	Pro	
				125				130						135	
Ile	Ser	Pro	Glu	Trp	Val	Arg	Thr	Arg	Pro	Phe	Pro	Ile	Leu	Pro	
				140				145						150	

Phe Pro Leu Gln Leu Phe Cys Phe Leu Val Ala Ile Arg Val Pro
155 160 165

Phe Pro Trp Thr Val Trp Arg Lys Thr Glu Ala Gly Val Trp Asp
170 175 180

<210> 294
<211> 1164
<212> DNA
<213> Homo sapiens

<400> 294
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cggcctaaga tgccacttct tctcatgtcc caggcttgag gccctgtggt 200

ccccatcctt gggagaagtc agctccagca ccatgaaggg catcctcgtt 250

gctggtatca ctgcagtgct tgttgcagct gtagaatctc tgagctgcgt 300

gcagtgtaat tcatgggaaa aatcctgtgt caacagcatt gcctctgaat 350

gtccctcaca tgccaacacc agctgtatca gctcctcagc cagctcctct 400

ctagagacac cagtcagatt ataccagaat atgttctgct cagcggagaa 450

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aacaccagcg atgccctgga ccctcccctg aagaacgtgt ccagcaacgc 600

agagtgccct gcttgttatg aatctaatgg aacttcctgt cgtgggaagc 650

cctggaaatg ctatgaagaa gaacagtgtg tctttctagt tgcagaactt 700

aagaatgaca ttgagtctaa gagtctcgtg ctgaaaggct gttccaacgt 750

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acgtctgcac caaccacttc ccacaacgtg ggctccaaag cttccctcta 900

cctcttggcc cttgccagcc tccttcttcg gggactgctg ccctgaggtc 950

ctggggctgc actttgccca gcaccccatt tctgcttctc tgaggtccag 1000

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ttgttcttca ttattaaagc actggttcat tcactgccaa aaaaaaaaaa 1150

aaaaaaaaaa aaaa 1164

<210> 295
<211> 237
<212> PRT

<213> Homo sapiens

<400> 295

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Met Lys Gly Ile Leu Val Ala Gly Ile Thr Ala Val Leu Val Ala
 1               5                  10                  15

Ala Val Glu Ser Leu Ser Cys Val Gln Cys Asn Ser Trp Glu Lys
            20                  25                  30

Ser Cys Val Asn Ser Ile Ala Ser Glu Cys Pro Ser His Ala Asn
        35                  40                  45

Thr Ser Cys Ile Ser Ser Ser Ala Ser Ser Ser Leu Glu Thr Pro
    50                  55                  60

Val Arg Leu Tyr Gln Asn Met Phe Cys Ser Ala Glu Asn Cys Ser
65                  70                  75

Glu Glu Thr His Ile Thr Ala Phe Thr Val His Val Ser Ala Glu
            80                  85                  90

Glu His Phe His Phe Val Ser Gln Cys Cys Gln Gly Lys Glu Cys
        95                  100                 105

Ser Asn Thr Ser Asp Ala Leu Asp Pro Pro Leu Lys Asn Val Ser
    110                 115                 120

Ser Asn Ala Glu Cys Pro Ala Cys Tyr Glu Ser Asn Gly Thr Ser
125                 130                 135

Cys Arg Gly Lys Pro Trp Lys Cys Tyr Glu Glu Glu Gln Cys Val
            140                 145                 150

Phe Leu Val Ala Glu Leu Lys Asn Asp Ile Glu Ser Lys Ser Leu
        155                 160                 165

Val Leu Lys Gly Cys Ser Asn Val Ser Asn Ala Thr Cys Gln Phe
    170                 175                 180

Leu Ser Gly Glu Asn Lys Thr Leu Gly Gly Val Ile Phe Arg Lys
185                 190                 195

Phe Glu Cys Ala Asn Val Asn Ser Leu Thr Pro Thr Ser Ala Pro
            200                 205                 210

Thr Thr Ser His Asn Val Gly Ser Lys Ala Ser Leu Tyr Leu Leu
        215                 220                 225

Ala Leu Ala Ser Leu Leu Leu Arg Gly Leu Leu Pro
    230                 235
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<210> 296
<211> 1245
<212> DNA
<213> Homo sapiens

<400> 296

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ccagccccat ggtccccgcc gccggcgcgc tgctgtgggt cctgctgctg 150
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aatctgggtc cccgggcggc gggggcccaa ggcctgaccc agactccgac 200

cgaaatgcag cgggtcagtt tacgctttgg gggccccatg acccgcagct 250

accggagcac cgcccggact ggtcttcccc ggaagacaag gataatccta 300

gaggacgaga atgatgccat ggccgacgcc gaccgcctgg ctggaccagc 350

ggctgccgag ctcttggccg ccacggtgtc caccggcttt agccggtcgt 400

ccgccattaa cgaggaggat gggtcttcag aagagggggt tgtgattaat 450

gccggaaagg atagcaccag cagagagctt cccagtgcga ctcccaatac 500

agcggggagt tccagcacga ggtttatagc caatagtcag gagcctgaaa 550

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atctgcggct ggtgctgatg ccctggggcc cgtggcactg ccactgcaag 750

tcgggcacca tgagccggag ccggtctggg aagctgcacg gcctttccgg 800

gcgccttcga gttggggcgc tgagccagct ccgcacggag cacaagcctt 850

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ccactagata tttttagtac agaaaaacaa aactggaaaa cacaa 1245

<210> 297
<211> 341
<212> PRT
<213> Homo sapiens

<400> 297

Met	Val	Pro	Ala	Ala	Gly	Ala	Leu	Leu	Trp	Val	Leu	Leu	Leu	Asn	
1				5				10					15		
Leu	Gly	Pro	Arg	Ala	Ala	Gly	Ala	Gln	Gly	Leu	Thr	Gln	Thr	Pro	
			20					25					30		
Thr	Glu	Met	Gln	Arg	Val	Ser	Leu	Arg	Phe	Gly	Gly	Pro	Met	Thr	
			35					40					45		
Arg	Ser	Tyr	Arg	Ser	Thr	Ala	Arg	Thr	Gly	Leu	Pro	Arg	Lys	Thr	
			50					55					60		
Arg	Ile	Ile	Leu	Glu	Asp	Glu	Asn	Asp	Ala	Met	Ala	Asp	Ala	Asp	

65 70 75

Arg Leu Ala Gly Pro Ala Ala Ala Glu Leu Leu Ala Ala Thr Val
80 85 90

Ser Thr Gly Phe Ser Arg Ser Ser Ala Ile Asn Glu Glu Asp Gly
95 100 105

Ser Ser Glu Glu Gly Val Val Ile Asn Ala Gly Lys Asp Ser Thr
110 115 120

Ser Arg Glu Leu Pro Ser Ala Thr Pro Asn Thr Ala Gly Ser Ser
125 130 135

Ser Thr Arg Phe Ile Ala Asn Ser Gln Glu Pro Glu Ile Arg Leu
140 145 150

Thr Ser Ser Leu Pro Arg Ser Pro Gly Arg Ser Thr Glu Asp Leu
155 160 165

Pro Gly Ser Gln Ala Thr Leu Ser Gln Trp Ser Thr Pro Gly Ser
170 175 180

Thr Pro Ser Arg Trp Pro Ser Pro Ser Pro Thr Ala Met Pro Ser
185 190 195

Pro Glu Asp Leu Arg Leu Val Leu Met Pro Trp Gly Pro Trp His
200 205 210

Cys His Cys Lys Ser Gly Thr Met Ser Arg Ser Arg Ser Gly Lys
215 220 225

Leu His Gly Leu Ser Gly Arg Leu Arg Val Gly Ala Leu Ser Gln
230 235 240

Leu Arg Thr Glu His Lys Pro Cys Thr Tyr Gln Gln Cys Pro Cys
245 250 255

Asn Arg Leu Arg Glu Glu Cys Pro Leu Asp Thr Ser Leu Cys Thr
260 265 270

Asp Thr Asn Cys Ala Ser Gln Ser Thr Thr Ser Thr Arg Thr Thr
275 280 285

Thr Thr Pro Phe Pro Thr Ile His Leu Arg Ser Ser Pro Ser Leu
290 295 300

Pro Pro Ala Ser Pro Cys Pro Ala Leu Ala Phe Trp Lys Arg Val
305 310 315

Arg Ile Gly Leu Glu Asp Ile Trp Asn Ser Leu Ser Ser Val Phe
320 325 330

Thr Glu Met Gln Pro Ile Asp Arg Asn Gln Arg
335 340

<210> 298
<211> 2692
<212> DNA
<213> Homo sapiens

<400> 298
cccgggtcga cccacgcgtc cggggagaaa ggatggccgg cctggcggcg 50

cggttggtcc tgctagctgg ggcagcggcg ctggcgagcg gctcccaggg 100

cgaccgtgag ccggtgtacc gcgactgcgt actgcagtgc gaagagcaga 150

actgctctgg gggcgctctg aatcacttcc gctcccgcca gccaatctac 200

atgagtctag caggctggac ctgtcgggac gactgtaagt atgagtgtat 250

gtgggtcacc gttgggctct acctccagga aggtcacaaa gtgcctcagt 300

tccatggcaa gtggcccttc tcccggttcc tgttctttca agagccggca 350

tcggccgtgg cctcgtttct caatggcctg gccagcctgg tgatgctctg 400

ccgctaccgc accttcgtgc cagcctcctc ccccatgtac cacacctgtg 450

tggccttcgc ctgggtgtcc ctcaatgcat ggttctggtc cacagtcttc 500

cacaccaggg acactgacct cacagagaaa atggactact tctgtgcctc 550

cactgtcatc ctacactcaa tctacctgtg ctgcgtcagg accgtggggc 600

tgcagcaccc agctgtggtc agtgccttcc gggctctcct gctgctcatg 650

ctgaccgtgc acgtctccta cctgagcctc atccgcttcg actatggcta 700

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ttggagcgag tctgccccag tggggatcct gcccccgccc tgctggcctc 1050

ccttctcccc tcaacccttg agatgatttt ctcttttcaa cttcttgaac 1100

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ttggccctca ccagccttgg agtctgttct agggaaggcc tcccagcatc 1200

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tgtgtgtgtg caggggggtgg gtgtgttagc gtgggttagg ggaacgtgtg 1850

tgcgcgtgct ggtgggcatg tgagatgagt gactgccggt gaatgtgtcc 1900

acagttgaga ggttggagca ggatgaggga atcctgtcac catcaataat 1950

cacttgtgga gcgccagctc tgcccaagac gccacctggg cggacagcca 2000

ggagctctcc atggccaggc tgcctgtgtg catgttccct gtctggtgcc 2050

cctttgcccg cctcctgcaa acctcacagg gtccccacac aacagtgccc 2100

tccagaagca gcccctcgga ggcagaggaa ggaaaatggg gatggctggg 2150

gctctctcca tcctcctttt ctccttgcct tcgcatggct ggccttcccc 2200

tccaaaacct ccattccccc gctgccagcc cctttgccat agcctgattt 2250

tggggaggag gaaggggcga tttgagggag aaggggagaa agcttatggc 2300

tgggtctggt ttcttccctt cccagagggt cttactgttc cagggtggcc 2350

ccagggcagg caggggccac actatgcctg tgccctggta aaggtgaccc 2400

ctgccattta ccagcagccc tggcatgttc ctgccccaca ggaatagaat 2450

ggagggagct ccagaaactt tccatcccaa aggcagtctc cgtggttgaa 2500

gcagactgga tttttgctct gcccctgacc ccttgtccct ctttgaggga 2550

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gcttcttttg atactgaaaa cttttaaggt gggagggtgg caagggatgt 2650

gcttaataaa tcaattccaa gcctcaaaaa aaaaaaaaaa aa 2692

<210> 299
<211> 320
<212> PRT
<213> Homo sapiens

<400> 299

Met Ala Gly Leu Ala Ala Arg Leu Val Leu Leu Ala Gly Ala Ala
1 5 10 15

Ala Leu Ala Ser Gly Ser Gln Gly Asp Arg Glu Pro Val Tyr Arg
20 25 30

Asp Cys Val Leu Gln Cys Glu Glu Gln Asn Cys Ser Gly Gly Ala
35 40 45

Leu Asn His Phe Arg Ser Arg Gln Pro Ile Tyr Met Ser Leu Ala
50 55 60

Gly Trp Thr Cys Arg Asp Asp Cys Lys Tyr Glu Cys Met Trp Val
65 70 75

Thr Val Gly Leu Tyr Leu Gln Glu Gly His Lys Val Pro Gln Phe
80 85 90

His Gly Lys Trp Pro Phe Ser Arg Phe Leu Phe Phe Gln Glu Pro
95 100 105

Ala Ser Ala Val Ala Ser Phe Leu Asn Gly Leu Ala Ser Leu Val
110 115 120

Met Leu Cys Arg Tyr Arg Thr Phe Val Pro Ala Ser Ser Pro Met
125 130 135

Tyr His Thr Cys Val Ala Phe Ala Trp Val Ser Leu Asn Ala Trp
140 145 150

Phe Trp Ser Thr Val Phe His Thr Arg Asp Thr Asp Leu Thr Glu
155 160 165

Lys Met Asp Tyr Phe Cys Ala Ser Thr Val Ile Leu His Ser Ile
170 175 180

Tyr Leu Cys Cys Val Arg Thr Val Gly Leu Gln His Pro Ala Val
185 190 195

Val Ser Ala Phe Arg Ala Leu Leu Leu Leu Met Leu Thr Val His
200 205 210

Val Ser Tyr Leu Ser Leu Ile Arg Phe Asp Tyr Gly Tyr Asn Leu
215 220 225

Val Ala Asn Val Ala Ile Gly Leu Val Asn Val Val Trp Trp Leu
230 235 240

Ala Trp Cys Leu Trp Asn Gln Arg Arg Leu Pro His Val Arg Lys
245 250 255

Cys Val Val Val Val Leu Leu Leu Gln Gly Leu Ser Leu Leu Glu
260 265 270

Leu Leu Asp Phe Pro Pro Leu Phe Trp Val Leu Asp Ala His Ala
275 280 285

Ile Trp His Ile Ser Thr Ile Pro Val His Val Leu Phe Phe Ser
290 295 300

Phe Leu Glu Asp Asp Ser Leu Tyr Leu Leu Lys Glu Ser Glu Asp
305 310 315

Lys Phe Lys Leu Asp
320

<210> 300
<211> 1674
<212> DNA
<213> Homo sapiens

<400> 300
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gaaggtccgt gactatggct ccccagagcc tgccttcatc taggatggct 100

cctctgggca tgctgcttgg gctgctgatg gccgcctgct tcaccttctg 150

cctcagtcat cagaacctga aggagtttgc cctgaccaac ccagagaaga 200

gcagcaccaa agaaacggag agaaaagaaa ccaaagccga ggaggagctg 250

gatgccgaag tcctggaggt gttccacccg acgcatgagt ggcaggccct 300

tcagccaggg caggctgtcc ctgcaggatc ccacgtacgg ctgaatcttc 350

agactgggga aagagaggca aaactccaat atgaggacaa gttccgaaat 400

aatttgaaag gcaaaaggct ggatatcaac accaacacct acacatctca 450

ggatctcaag agtgcactgg caaaattcaa ggaggggggca gagatggaga 500

gttcaaagga agacaaggca aggcaggctg aggtaaagcg gctcttccgc 550

cccattgagg aactgaagaa agactttgat gagctgaatg ttgtcattga 600

gactgacatg cagatcatgg tacggctgat caacaagttc aatagttcca 650

gctccagttt ggaagagaag attgctgcgc tctttgatct tgaatattat 700

gtccatcaga tggacaatgc gcaggacctg ctttcctttg gtggtcttca 750

agtggtgatc aatgggctga acagcacaga gcccctcgtg aaggagtatg 800

ctgcgtttgt gctgggcgct gccttttcca gcaaccccaa ggtccaggtg 850

gaggccatcg aaggggggagc cctgcagaag ctgctggtca tcctggccac 900

ggagcagccg ctcactgcaa agaagaaggt cctgtttgca ctgtgctccc 950

tgctgcgcca cttcccctat gcccagcggc agttcctgaa gctcgggggg 1000

ctgcaggtcc tgaggaccct ggtgcaggag aagggcacgg aggtgctcgc 1050

cgtgcgcgtg gtcacactgc tctacgacct ggtcacggag aagatgttcg 1100

ccgaggagga ggctgagctg acccaggaga tgtccccaga gaagctgcag 1150

cagtatcgcc aggtacacct cctgccaggc ctgtgggaac agggctggtg 1200

cgagatcacg gcccacctcc tggcgctgcc cgagcatgat gcccgtgaga 1250

aggtgctgca gacactgggc gtcctcctga ccacctgccg ggaccgctac 1300

cgtcaggacc cccagctcgg caggacactg gccagcctgc aggctgagta 1350

ccaggtgctg gccagcctgg agctgcagga tggtgaggac gagggctact 1400

tccaggagct gctgggctct gtcaacagct tgctgaagga gctgagatga 1450

ggccccacac caggactgga ctgggatgcc gctagtgagg ctgaggggtg 1500

ccagcgtggg tgggcttctc aggcaggagg acatcttggc agtgctggct 1550

tggccattaa atggaaacct gaaggccaaa aaaaaaaaaa aaaaaaaaaa 1600

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650

aaaaaaaaaa aaaaaaaaaa aaaa 1674

<210> 301

<211> 461
<212> PRT
<213> Homo sapiens

<400> 301
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Met Leu Leu Gly Leu Leu Met Ala Ala Cys Phe Thr Phe Cys Leu
20 25 30

Ser His Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys
35 40 45

Ser Ser Thr Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu
50 55 60

Glu Leu Asp Ala Glu Val Leu Glu Val Phe His Pro Thr His Glu
65 70 75

Trp Gln Ala Leu Gln Pro Gly Gln Ala Val Pro Ala Gly Ser His
80 85 90

Val Arg Leu Asn Leu Gln Thr Gly Glu Arg Glu Ala Lys Leu Gln
95 100 105

Tyr Glu Asp Lys Phe Arg Asn Asn Leu Lys Gly Lys Arg Leu Asp
110 115 120

Ile Asn Thr Asn Thr Tyr Thr Ser Gln Asp Leu Lys Ser Ala Leu
125 130 135

Ala Lys Phe Lys Glu Gly Ala Glu Met Glu Ser Ser Lys Glu Asp
140 145 150

Lys Ala Arg Gln Ala Glu Val Lys Arg Leu Phe Arg Pro Ile Glu
155 160 165

Glu Leu Lys Lys Asp Phe Asp Glu Leu Asn Val Val Ile Glu Thr
170 175 180

Asp Met Gln Ile Met Val Arg Leu Ile Asn Lys Phe Asn Ser Ser
185 190 195

Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala Leu Phe Asp Leu Glu
200 205 210

Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp Leu Leu Ser Phe
215 220 225

Gly Gly Leu Gln Val Val Ile Asn Gly Leu Asn Ser Thr Glu Pro
230 235 240

Leu Val Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala Ala Phe Ser
245 250 255

Ser Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Gly Ala Leu
260 265 270

Gln Lys Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr Ala
275 280 285

Lys Lys Lys Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe

290 295 300

Pro Tyr Ala Gln Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val
305 310 315

Leu Arg Thr Leu Val Gln Glu Lys Gly Thr Glu Val Leu Ala Val
320 325 330

Arg Val Val Thr Leu Leu Tyr Asp Leu Val Thr Glu Lys Met Phe
335 340 345

Ala Glu Glu Glu Ala Glu Leu Thr Gln Glu Met Ser Pro Glu Lys
350 355 360

Leu Gln Gln Tyr Arg Gln Val His Leu Leu Pro Gly Leu Trp Glu
365 370 375

Gln Gly Trp Cys Glu Ile Thr Ala His Leu Leu Ala Leu Pro Glu
380 385 390

His Asp Ala Arg Glu Lys Val Leu Gln Thr Leu Gly Val Leu Leu
395 400 405

Thr Thr Cys Arg Asp Arg Tyr Arg Gln Asp Pro Gln Leu Gly Arg
410 415 420

Thr Leu Ala Ser Leu Gln Ala Glu Tyr Gln Val Leu Ala Ser Leu
425 430 435

Glu Leu Gln Asp Gly Glu Asp Glu Gly Tyr Phe Gln Glu Leu Leu
440 445 450

Gly Ser Val Asn Ser Leu Leu Lys Glu Leu Arg
455 460

<210> 302
<211> 2136
<212> DNA
<213> Homo sapiens

<400> 302
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cccccccttc cccttccccg gggtctgggg gtgacattgc accgcgcccc 100

tcgtggggtc gcgttgccac cccacgcgga ctccccagct ggcgcgcccc 150

tcccatttgc ctgtcctggt caggccccca ccccccttcc cacctgacca 200

gccatggggg ctgcggtgtt tttcggctgc actttcgtcg cgttcggccc 250

ggccttcgcg cttttcttga tcactgtggc tggggacccg cttcgcgtta 300

tcatcctggt cgcaggggca ttttttctggc tggtctccct gctcctggcc 350

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gctccagtac ggcctcctga tttttggtgc tgctgtctct gtccttctac 450

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gggttagcat cgctgagtga ggacggaaga tcacccatct ccatccgcca 550

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ctgttatcaa tattttggct gatgcacttg ggccaggtgt ggttgggatc 650

catggagact caccctatta cttcctgact tcagcctttc tgacagcagc 700

cattatcctg ctccatacct tttggggagt tgtgttcttt gatgcctgtg 750

agaggagacg gtactgggct ttgggcctgg tggttgggag tcacctactg 800

acatcgggac tgacattcct gaacccctgg tatgaggcca gcctgctgcc 850

catctatgca gtcactgttt ccatggggct ctgggccttc atcacagctg 900

gagggtccct ccgaagtatt cagcgcagcc tcttgtgtaa ggactgacta 950

cctggactga tcgcctgaca gatcccacct gcctgtccac tgcccatgac 1000

tgagcccagc cccagccccgg gtccattgcc cacattctct gtctccttct 1050

cgtcggtcta ccccactacc tccagggttt tgctttgtcc ttttgtgacc 1100

gttagtctct aagctttacc aggagcagcc tgggttcagc cagtcagtga 1150

ctggtgggtt tgaatctgca cttatcccca ccacctgggg acccccttgt 1200

tgtgtccagg actccccctg tgtcagtgct ctgctctcac cctgcccaag 1250

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ctcatttcgg tccctttctc cttggtccca gaccttgggg gaaaggaagg 1750

aagtgcatgt ttgggaactg gcattactgg aactaatggt tttaacctcc 1800

ttaaccacca gcatccctcc tctccccaag gtgaagtgga gggtgctgtg 1850

gtgagctggc cactccagag ctgcagtgcc actggaggag tcagactacc 1900

atgacatcgt agggaaggag gggagatttt tttgtagttt ttaattgggg 1950

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ggtggagtgt cccatccttt taatcaaggt gattgtgatt ttgactaata 2050

aaaaagaatt tgtaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2100

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2136

<210> 303
<211> 247
<212> PRT
<213> Homo sapiens

<400> 303
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1 5 10 15

Pro Ala Phe Ala Leu Phe Leu Ile Thr Val Ala Gly Asp Pro Leu
20 25 30

Arg Val Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser
35 40 45

Leu Leu Leu Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr
50 55 60

Asp Arg Ser Asp Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly
65 70 75

Ala Ala Val Ser Val Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr
80 85 90

Tyr Lys Leu Leu Lys Lys Ala Asp Glu Gly Leu Ala Ser Leu Ser
95 100 105

Glu Asp Gly Arg Ser Pro Ile Ser Ile Arg Gln Met Ala Tyr Val
110 115 120

Ser Gly Leu Ser Phe Gly Ile Ile Ser Gly Val Phe Ser Val Ile
125 130 135

Asn Ile Leu Ala Asp Ala Leu Gly Pro Gly Val Val Gly Ile His
140 145 150

Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser Ala Phe Leu Thr Ala
155 160 165

Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val Val Phe Phe Asp
170 175 180

Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu Gly Leu Val Val Gly
185 190 195

Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro Trp Tyr
200 205 210

Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met Gly
215 220 225

Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln
230 235 240

Arg Ser Leu Leu Cys Lys Asp
245

<210> 304
<211> 240
<212> DNA
<213> Homo sapiens

<220>

<221> unsure
<222> 108, 123, 126, 154, 198, 206, 217
<223> unknown base

<400> 304
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aagatcaacc catttccatt ccgccagatg gcctatgttt ctggtctctc 100

ccttcggnat catcagtggt gtnttntctg ttatcaatat tttggctgat 150

gcanttgggc caggtgtggt tgggatccat ggagactcac cctattantt 200

cctganttca gcctttntga cagcagccat tatcctgctc 240

<210> 305
<211> 378
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 58, 94, 132, 186, 191, 220, 240, 248, 280, 311, 332
<223> unknown base

<400> 305
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ctgctgtntc tgtccttcta caggaggtgt tccgctttgc ctantacaag 100

ctgcttaaga aggcagatga ggggttagca tngctgagtg aggacggaag 150

atcacccatt tccatccgcc agatggccta tgtttntggt ntttccttcg 200

gtatcatcag tggtgttttn tctgttatca atattttggn tgatgcantt 250

gggccaggtg tggttgggat ccatggagan tcaccctatt aattcctgaa 300

ttcagccttt ntgacagcag ccattatcct gntccatacc ttttggggag 350

ttgtgttttt tgatgcctgt gagaggag 378

<210> 306
<211> 655
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1, 22, 129, 133, 184
<223> unknown base

<400> 306
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gcgttgccac cccacgcgga ctccccagnt ggngcgccct tcccatttgc 150

ctgtcctggt caggcccccа ccccccttcc cacntgacca gccatggggg 200

ctgcggtgtt tttcggctgc actttcgtcg cgttcggccc ggccttcgcg 250

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ccgctttgcc tactacaagc tgcttaagaa ggcagatgag gggttagcat 500

cgctgagtga ggacggaaga tcacccatct ccatccgcca gatggcctat 550

gtttctggtc tctccttcgg tatcatcagt ggtgtcttct ctgttatcaa 600

tattttggct gatgcacttg ggccaggtgt ggttgggatc catggagact 650

caccc 655

<210> 307
<211> 650
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 52, 89, 128
<223> unknown base

<400> 307
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cgttgccacc ccacgcggac tccccagntg gcgcgcccct cccatttgcc 150

tgtcctggtc aggcccccac ccccttcccc acctgaccag ccatgggggc 200

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tggttcatct tggtccatgt gaccgaccgg tcagatgccc ggctccagta 400

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tgtttctggt ctctccttcg gtatcatcag tggtgtcttc tctgttatca 600

atattttggc tgatgcactt gggccaggtg tggttgggat ccatggagac 650

<210> 308
<211> 1570
<212> DNA
<213> Homo sapiens

<400> 308
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aggaggaggc agtggccagg aaggcacagg cctgagaagt ctgcggctga 100

gctgggagca aatcccccac cccctacctg ggggacaggg caagtgagac 150

ctggtgaggg tggctcagca ggcagggaag gagaggtgtc tgtgcgtcct 200

gcacccacat ctttctctgt cccctccttg ccctgtctgg aggctgctag 250

actcctatct tctgaattct atagtgcctg ggtctcagcg cagtgccgat 300

ggtggcccgt ccttgtggtt cctctctacc tggggaaata aggtgcagcg 350

gccatggcta cagcaagacc cccctggatg tgggtgctct gtgctctgat 400

cacagccttg cttctggggg tcacagagca tgttctcgcc aacaatgatg 450

tttcctgtga ccacccctct aacaccgtgc cctctgggag caaccaggac 500

ctgggagctg gggccgggga agacgcccgg tcggatgaca gcagcagccg 550

catcatcaat ggatccgact gcgatatgca cacccagccg tggcaggccg 600

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gcgggggttg cgtctcaatc tccctggggc actttcatcc tcaagctcag 1500

ggcccatccc ttctctgcag ctctgaccca aatttagtcc cagaaataaa 1550

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<210> 309

<211> 293
<212> PRT
<213> Homo sapiens

<400> 309

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Met Ala Thr Ala Arg Pro Pro Trp Met Trp Val Leu Cys Ala Leu
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Ile Thr Ala Leu Leu Leu Gly Val Thr Glu His Val Leu Ala Asn
             20                  25                  30

Asn Asp Val Ser Cys Asp His Pro Ser Asn Thr Val Pro Ser Gly
             35                  40                  45

Ser Asn Gln Asp Leu Gly Ala Gly Ala Gly Glu Asp Ala Arg Ser
             50                  55                  60

Asp Asp Ser Ser Ser Arg Ile Ile Asn Gly Ser Asp Cys Asp Met
             65                  70                  75

His Thr Gln Pro Trp Gln Ala Ala Leu Leu Leu Arg Pro Asn Gln
             80                  85                  90

Leu Tyr Cys Gly Ala Val Leu Val His Pro Gln Trp Leu Leu Thr
             95                 100                 105

Ala Ala His Cys Arg Lys Lys Val Phe Arg Val Arg Leu Gly His
            110                 115                 120

Tyr Ser Leu Ser Pro Val Tyr Glu Ser Gly Gln Gln Met Phe Gln
            125                 130                 135

Gly Val Lys Ser Ile Pro His Pro Gly Tyr Ser His Pro Gly His
            140                 145                 150

Ser Asn Asp Leu Met Leu Ile Lys Leu Asn Arg Arg Ile Arg Pro
            155                 160                 165

Thr Lys Asp Val Arg Pro Ile Asn Val Ser Ser His Cys Pro Ser
            170                 175                 180

Ala Gly Thr Lys Cys Leu Val Ser Gly Trp Gly Thr Thr Lys Ser
            185                 190                 195

Pro Gln Val His Phe Pro Lys Val Leu Gln Cys Leu Asn Ile Ser
            200                 205                 210

Val Leu Ser Gln Lys Arg Cys Glu Asp Ala Tyr Pro Arg Gln Ile
            215                 220                 225

Asp Asp Thr Met Phe Cys Ala Gly Asp Lys Ala Gly Arg Asp Ser
            230                 235                 240

Cys Gln Gly Asp Ser Gly Gly Pro Val Val Cys Asn Gly Ser Leu
            245                 250                 255

Gln Gly Leu Val Ser Trp Gly Asp Tyr Pro Cys Ala Arg Pro Asn
            260                 265                 270

Arg Pro Gly Val Tyr Thr Asn Leu Cys Lys Phe Thr Lys Trp Ile
            275                 280                 285

Gln Glu Thr Ile Gln Ala Asn Ser
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<210> 310
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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 310
tcctgtgacc acccctctaa cacc 24

<210> 311
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 311
ctggaacatc tgctgcccag attc 24

<210> 312
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 312
gtcggatgac agcagcagcc gcatcatcaa tggatccgac tgcgatatgc 50

<210> 313
<211> 3010
<212> DNA
<213> Homo sapiens

<400> 313
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ccggccgcgc gacaagccgc agcggccgag ctgcggctac gtgctgtgca 100

ccgtgctgct ggccctggct gtgctgctgg ctgtagctgt caccggtgcc 150

gtgctcttcc tgaaccacgc ccacgcgccg ggcacggcgc ccccacctgt 200

cgtcagcact ggggctgcca gcgccaacag cgccctggtc actgtggaaa 250

gggcggacag ctcgcacctc agcatcctca ttgacccgcg ctgccccgac 300

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ggcgctgaca gagcaccagg cccagccacg gctggtgggc gaccaggagc 400

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<210> 314
<211> 461
<212> PRT
<213> Homo sapiens

<400> 314

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Glu	Asp	Arg	Pro	Arg	Asp	Lys	Pro	Gln	Arg	Pro	Ser	Cys	Gly	Tyr	
				20				25						30	
Val	Leu	Cys	Thr	Val	Leu	Leu	Ala	Leu	Ala	Val	Leu	Leu	Ala	Val	
				35				40						45	
Ala	Val	Thr	Gly	Ala	Val	Leu	Phe	Leu	Asn	His	Ala	His	Ala	Pro	
				50				55						60	
Gly	Thr	Ala	Pro	Pro	Pro	Val	Val	Ser	Thr	Gly	Ala	Ala	Ser	Ala	
				65				70						75	
Asn	Ser	Ala	Leu	Val	Thr	Val	Glu	Arg	Ala	Asp	Ser	Ser	His	Leu	
				80				85						90	
Ser	Ile	Leu	Ile	Asp	Pro	Arg	Cys	Pro	Asp	Leu	Thr	Asp	Ser	Phe	
				95				100						105	

Ala Arg Leu Glu Ser Ala Gln Ala Ser Val Leu Gln Ala Leu Thr
110 115 120

Glu His Gln Ala Gln Pro Arg Leu Val Gly Asp Gln Glu Gln Glu
125 130 135

Leu Leu Asp Thr Leu Ala Asp Gln Leu Pro Arg Leu Leu Ala Arg
140 145 150

Ala Ser Glu Leu Gln Thr Glu Cys Met Gly Leu Arg Lys Gly His
155 160 165

Gly Thr Leu Gly Gln Gly Leu Ser Ala Leu Gln Ser Glu Gln Gly
170 175 180

Arg Leu Ile Gln Leu Leu Ser Glu Ser Gln Gly His Met Ala His
185 190 195

Leu Val Asn Ser Val Ser Asp Ile Leu Asp Ala Leu Gln Arg Asp
200 205 210

Arg Gly Leu Gly Arg Pro Arg Asn Lys Ala Asp Leu Gln Arg Ala
215 220 225

Pro Ala Arg Gly Thr Arg Pro Arg Gly Cys Ala Thr Gly Ser Arg
230 235 240

Pro Arg Asp Cys Leu Asp Val Leu Leu Ser Gly Gln Gln Asp Asp
245 250 255

Gly Val Tyr Ser Val Phe Pro Thr His Tyr Pro Ala Gly Phe Gln
260 265 270

Val Tyr Cys Asp Met Arg Thr Asp Gly Gly Gly Trp Thr Val Phe
275 280 285

Gln Arg Arg Glu Asp Gly Ser Val Asn Phe Phe Arg Gly Trp Asp
290 295 300

Ala Tyr Arg Asp Gly Phe Gly Arg Leu Thr Gly Glu His Trp Leu
305 310 315

Gly Leu Lys Arg Ile His Ala Leu Thr Thr Gln Ala Ala Tyr Glu
320 325 330

Leu His Val Asp Leu Glu Asp Phe Glu Asn Gly Thr Ala Tyr Ala
335 340 345

Arg Tyr Gly Ser Phe Gly Val Gly Leu Phe Ser Val Asp Pro Glu
350 355 360

Glu Asp Gly Tyr Pro Leu Thr Val Ala Asp Tyr Ser Gly Thr Ala
365 370 375

Gly Asp Ser Leu Leu Lys His Ser Gly Met Arg Phe Thr Thr Lys
380 385 390

Asp Arg Asp Ser Asp His Ser Glu Asn Asn Cys Ala Ala Phe Tyr
395 400 405

Arg Gly Ala Trp Trp Tyr Arg Asn Cys His Thr Ser Asn Leu Asn
410 415 420

Gly Gln Tyr Leu Arg Gly Ala His Ala Ser Tyr Ala Asp Gly Val
425 430 435

Glu Trp Ser Ser Trp Thr Gly Trp Gln Tyr Ser Leu Lys Phe Ser
440 445 450

Glu Met Lys Ile Arg Pro Val Arg Glu Asp Arg
455 460

<210> 315
<211> 24
<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 315
cacacgtcca acctcaatgg gcag 24

<210> 316
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 316
gaccagcagg gccaaggaca agg 23

<210> 317
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 317
gttctctgag atgaagatcc ggccggtccg ggagtaccgc ttag 44

<210> 318
<211> 1841
<212> DNA
<213> Homo sapiens

<400> 318
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<210> 319
<211> 280
<212> PRT
<213> Homo sapiens

<400> 319

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Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Asp
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Gly Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr
             20                  25                  30

Arg His Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser
             35                  40                  45

Thr Trp Arg Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val
             50                  55                  60

Leu Leu Ile Gly Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr
             65                  70                  75

Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr Ile Ser Gln Met Glu
             80                  85                  90

Glu Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln Ser Leu Gln Val
             95                 100                 105

Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln His Val Ala Glu Lys
            110                 115                 120

Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Ala His Arg Cys Ser
            125                 130                 135

Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln
            140                 145                 150

Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys
            155                 160                 165

Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp
            170                 175                 180

Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser
            185                 190                 195

Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu
            200                 205                 210

Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile
            215                 220                 225

Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu
            230                 235                 240

Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys
            245                 250                 255

Val Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His
            260                 265                 270

Val Pro Pro Glu Thr Leu Gly Glu Gly Asp
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<210> 320
<211> 468
<212> DNA
<213> Homo sapiens

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<221> unsure
<222> 59, 95, 149, 331, 364, 438, 446
<223> unknown base

<400> 320
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ttaggaaata cgtcccaaga gttgcaattt nttcaagtcc agaatataaa 350

gcttgcagga agtntgcagc atgtggctga aaaactctgt cgtgagctgt 400

ataacaaagc tggaggaact ttgaaggagg gcaaagtntc ctcatntact 450

atacacacac cacttccc 468

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<210> 322
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<220>
<223> Synthetic oligonucleotide probe

<400> 322
catgctgacg acttcctgca agc 23

<210> 323
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<220>
<223> Synthetic oligonucleotide probe

<400> 323
ccacacagtc tctgcttctt ggg 23

<210> 324
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<223> Synthetic oligonucleotide probe

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<210> 325
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<212> DNA
<213> Homo sapiens

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cacactgttc ctgctggccg ggccagacac ggtgctcacg cctgacttcc 2100

tgaaccgctg ccgcatgcat gccatctccg gctggcaggc cttctttccc 2150

atgcatttcc aagccttcca cccaggtgtg gccccaccac aagggcctgg 2200

gcccccagag ctgggccgtg acactggccg ctttgatcgc caggcagcca 2250

gcgaggcctg cttctacaac tccgactacg tggcagcccg tgggcgcctg 2300

gcggcagcct cagaacaaga agaggagctg ctggagagcc tggatgtgta 2350

cgagctgttc ctccacttct ccagtctgca tgtgctgcgg gcggtggagc 2400

cggcgctgct gcagcgctac cgggcccaga cgtgcagcgc gaggctcagt 2450

gaggacctgt accaccgctg cctccagagc gtgcttgagg gcctcggctc 2500

ccgaacccag ctggccatgc tactctttga acaggagcag ggcaacagca 2550

cctgacccca ccctgtcccc gtgggccgtg gcatggccac accccacccc 2600

acttctcccc caaaaccaga gccacctgcc agcctcgctg ggcagggctg 2650

gccgtagcca gaccccaagc tggcccactg gtcccctctc tggctctgtg 2700

ggtccctggg ctctggacaa gcactggggg acgtgccccc agagccaccc 2750

acttctcatc ccaaacccag tttccctgcc ccctgacgct gctgattcgg 2800

gctgtggcct ccacgtattt atgcagtaca gtctgcctga cgccagccct 2850

gcctctgggc cctgggggct gggctgtaga agagttgttg gggaaggagg 2900

gagctgagga gggggcatct cccaacttct ccctttgga ccctgccgaa 2950

gctccctgcc tttaataaac tggccaagtg tggaaaaa 2988

<210> 326
<211> 775
<212> PRT
<213> Homo sapiens

<400> 326

Met	Arg	Ala	Ser	Leu	Leu	Leu	Ser	Val	Leu	Arg	Pro	Ala	Gly	Pro	
1				5				10						15	
Val	Ala	Val	Gly	Ile	Ser	Leu	Gly	Phe	Thr	Leu	Ser	Leu	Leu	Ser	
				20				25						30	
Val	Thr	Trp	Val	Glu	Glu	Pro	Cys	Gly	Pro	Gly	Pro	Pro	Gln	Pro	
				35				40						45	
Gly	Asp	Ser	Glu	Leu	Pro	Pro	Arg	Gly	Asn	Thr	Asn	Ala	Ala	Arg	
				50				55						60	
Arg	Pro	Asn	Ser	Val	Gln	Pro	Gly	Ala	Glu	Arg	Glu	Lys	Pro	Gly	
				65				70						75	
Ala	Gly	Glu	Gly	Ala	Gly	Glu	Asn	Trp	Glu	Pro	Arg	Val	Leu	Pro	
				80				85						90	
Tyr	His	Pro	Ala	Gln	Pro	Gly	Gln	Ala	Ala	Lys	Lys	Ala	Val	Arg	
				95				100						105	
Thr	Arg	Tyr	Ile	Ser	Thr	Glu	Leu	Gly	Ile	Arg	Gln	Arg	Leu	Leu	
				110				115						120	
Val	Ala	Val	Leu	Thr	Ser	Gln	Thr	Thr	Leu	Pro	Thr	Leu	Gly	Val	
				125				130						135	
Ala	Val	Asn	Arg	Thr	Leu	Gly	His	Arg	Leu	Glu	Arg	Val	Val	Phe	
				140				145						150	
Leu	Thr	Gly	Ala	Arg	Gly	Arg	Arg	Ala	Pro	Pro	Gly	Met	Ala	Val	
				155				160						165	
Val	Thr	Leu	Gly	Glu	Glu	Arg	Pro	Ile	Gly	His	Leu	His	Leu	Ala	
				170				175						180	
Leu	Arg	His	Leu	Leu	Glu	Gln	His	Gly	Asp	Asp	Phe	Asp	Trp	Phe	
				185				190						195	
Phe	Leu	Val	Pro	Asp	Thr	Thr	Tyr	Thr	Glu	Ala	His	Gly	Leu	Ala	
				200				205						210	
Arg	Leu	Thr	Gly	His	Leu	Ser	Leu	Ala	Ser	Ala	Ala	His	Leu	Tyr	
				215				220						225	
Leu	Gly	Arg	Pro	Gln	Asp	Phe	Ile	Gly	Gly	Glu	Pro	Thr	Pro	Gly	
				230				235						240	
Arg	Tyr	Cys	His	Gly	Gly	Phe	Gly	Val	Leu	Leu	Ser	Arg	Met	Leu	
				245				250						255	
Leu	Gln	Gln	Leu	Arg	Pro	His	Leu	Glu	Gly	Cys	Arg	Asn	Asp	Ile	
				260				265						270	

Val Ser Ala Arg Pro Asp Glu Trp Leu Gly Arg Cys Ile Leu Asp
275 280 285

Ala Thr Gly Val Gly Cys Thr Gly Asp His Glu Gly Val His Tyr
290 295 300

Ser His Leu Glu Leu Ser Pro Gly Glu Pro Val Gln Glu Gly Asp
305 310 315

Pro His Phe Arg Ser Ala Leu Thr Ala His Pro Val Arg Asp Pro
320 325 330

Val His Met Tyr Gln Leu His Lys Ala Phe Ala Arg Ala Glu Leu
335 340 345

Glu Arg Thr Tyr Gln Glu Ile Gln Glu Leu Gln Trp Glu Ile Gln
350 355 360

Asn Thr Ser His Leu Ala Val Asp Gly Asp Arg Ala Ala Ala Trp
365 370 375

Pro Val Gly Ile Pro Ala Pro Ser Arg Pro Ala Ser Arg Phe Glu
380 385 390

Val Leu Arg Trp Asp Tyr Phe Thr Glu Gln His Ala Phe Ser Cys
395 400 405

Ala Asp Gly Ser Pro Arg Cys Pro Leu Arg Gly Ala Asp Arg Ala
410 415 420

Asp Val Ala Asp Val Leu Gly Thr Ala Leu Glu Glu Leu Asn Arg
425 430 435

Arg Tyr His Pro Ala Leu Arg Leu Gln Lys Gln Gln Leu Val Asn
440 445 450

Gly Tyr Arg Arg Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu
455 460 465

Asp Leu Gln Leu Glu Ala Leu Thr Pro Gln Gly Gly Arg Arg Pro
470 475 480

Leu Thr Arg Arg Val Gln Leu Leu Arg Pro Leu Ser Arg Val Glu
485 490 495

Ile Leu Pro Val Pro Tyr Val Thr Glu Ala Ser Arg Leu Thr Val
500 505 510

Leu Leu Pro Leu Ala Ala Ala Glu Arg Asp Leu Ala Pro Gly Phe
515 520 525

Leu Glu Ala Phe Ala Thr Ala Ala Leu Glu Pro Gly Asp Ala Ala
530 535 540

Ala Ala Leu Thr Leu Leu Leu Leu Tyr Glu Pro Arg Gln Ala Gln
545 550 555

Arg Val Ala His Ala Asp Val Phe Ala Pro Val Lys Ala His Val
560 565 570

Ala Glu Leu Glu Arg Arg Phe Pro Gly Ala Arg Val Pro Trp Leu
575 580 585

Ser Val Gln Thr Ala Ala Pro Ser Pro Leu Arg Leu Met Asp Leu
590 595 600

Leu Ser Lys Lys His Pro Leu Asp Thr Leu Phe Leu Leu Ala Gly
605 610 615

Pro Asp Thr Val Leu Thr Pro Asp Phe Leu Asn Arg Cys Arg Met
620 625 630

His Ala Ile Ser Gly Trp Gln Ala Phe Phe Pro Met His Phe Gln
635 640 645

Ala Phe His Pro Gly Val Ala Pro Pro Gln Gly Pro Gly Pro Pro
650 655 660

Glu Leu Gly Arg Asp Thr Gly Arg Phe Asp Arg Gln Ala Ala Ser
665 670 675

Glu Ala Cys Phe Tyr Asn Ser Asp Tyr Val Ala Ala Arg Gly Arg
680 685 690

Leu Ala Ala Ala Ser Glu Gln Glu Glu Leu Leu Glu Ser Leu
695 700 705

Asp Val Tyr Glu Leu Phe Leu His Phe Ser Ser Leu His Val Leu
710 715 720

Arg Ala Val Glu Pro Ala Leu Leu Gln Arg Tyr Arg Ala Gln Thr
725 730 735

Cys Ser Ala Arg Leu Ser Glu Asp Leu Tyr His Arg Cys Leu Gln
740 745 750

Ser Val Leu Glu Gly Leu Gly Ser Arg Thr Gln Leu Ala Met Leu
755 760 765

Leu Phe Glu Gln Glu Gln Gly Asn Ser Thr
770 775

<210> 327
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 327
tggaaggctg ccgcaacgac aatc 24

<210> 328
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 328
ctgatgtggc cgatgttctg 20

<210> 329
<211> 20

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 329
atggctcagt gtgcagacag 20

<210> 330
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 330
gcatgctgct ccgtgaagta gtcc 24

<210> 331
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 331
atgcatggga aagaaggcct gccc 24

<210> 332
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 332
tgcactggtg accacgaggg ggtgcactat agccatctgg agctgag 47

<210> 333
<211> 1095
<212> DNA
<213> Homo sapiens

<400> 333
gctctggccg gccccggcga ttggtcaccg cccgctaggg gacagccctg 50

gcctcctctg attggcaagc gctggccacc tccccacacc ccttgcgaac 100

gctcccctag tggagaaaag gagtagctat tagccaattc ggcagggccc 150

gcttttaga agcttgattt cctttgaaga tgaaagacta gcggaagctc 200

tgcctctttc cccagtgggc gagggaactc ggggcgattg gctgggaact 250

gtatccaccc aaatgtcacc gatttcttcc tatgcaggaa atgagcagac 300

ccatcaataa gaaatttctc agcctggccg aaaatggttg gccccacgaa 350

gccacgacaa ctggaggcaa agagggttgc tcaacgcccc gcctcattgg 400

aaaaccaaat cagatctggg acctatatag cgtggcggag gcggggcgat 450

gattgtcgcg ctcgcaccca ctgcagctgc gcacagtcgc atttctttcc 500

ccgcccctga gaccctgcag caccatctgt catggcggct gggctgtttg 550

gtttgagcgc tcgccgtctt ttggcggcag cggcgacgcg agggctcccg 600

gccgcccgcg tccgctggga atctagcttc tccaggactg tggtcgcccc 650

gtccgctgtg gcgggaaagc ggcccccaga accgaccaca ccgtggcaag 700

aggacccaga acccgaggac gaaaacttgt atgagaagaa cccagactcc 750

catggttatg acaaggaccc cgttttggac gtctggaaca tgcgacttgt 800

cttcttcttt ggcgtctcca tcatcctggt ccttggcagc acctttgtgg 850

cctatctgcc tgactacagg atgaaagagt ggtcccgccg cgaagctgag 900

aggcttgtga aataccgaga ggccaatggc cttcccatca tggaatccaa 950

ctgcttcgac cccagcaaga tccagctgcc agaggatgag tgaccagttg 1000

ctaagtgggg ctcaagaagc accgccttcc ccacccccctg cctgccattc 1050

tgacctcttc tcagagcacc taattaaagg ggctgaaagt ctgaa 1095

<210> 334
<211> 153
<212> PRT
<213> Homo sapiens

<400> 334

Met	Ala	Ala	Gly	Leu	Phe	Gly	Leu	Ser	Ala	Arg	Arg	Leu	Leu	Ala	
1				5				10						15	
Ala	Ala	Ala	Thr	Arg	Gly	Leu	Pro	Ala	Ala	Arg	Val	Arg	Trp	Glu	
			20					25						30	
Ser	Ser	Phe	Ser	Arg	Thr	Val	Val	Ala	Pro	Ser	Ala	Val	Ala	Gly	
			35					40						45	
Lys	Arg	Pro	Pro	Glu	Pro	Thr	Thr	Pro	Trp	Gln	Glu	Asp	Pro	Glu	
			50					55						60	
Pro	Glu	Asp	Glu	Asn	Leu	Tyr	Glu	Lys	Asn	Pro	Asp	Ser	His	Gly	
			65					70						75	
Tyr	Asp	Lys	Asp	Pro	Val	Leu	Asp	Val	Trp	Asn	Met	Arg	Leu	Val	
			80					85						90	
Phe	Phe	Phe	Gly	Val	Ser	Ile	Ile	Leu	Val	Leu	Gly	Ser	Thr	Phe	
			95					100						105	
Val	Ala	Tyr	Leu	Pro	Asp	Tyr	Arg	Met	Lys	Glu	Trp	Ser	Arg	Arg	
			110					115						120	
Glu	Ala	Glu	Arg	Leu	Val	Lys	Tyr	Arg	Glu	Ala	Asn	Gly	Leu	Pro	
			125					130						135	
Ile	Met	Glu	Ser	Asn	Cys	Phe	Asp	Pro	Ser	Lys	Ile	Gln	Leu	Pro	
			140					145						150	

Glu Asp Glu

<210> 335
<211> 442
<212> DNA
<213> Homo sapiens

<400> 335
ggcggctggg ctgtttggtt tgagcgctcg ccgtcttttg gcggcagcgg 50

cgacgcgagg gctcccggcc gcccgcgtcc gctgggaatc tagcttctcc 100

aggactgtgg tcgccccgtc cgctgtggcg ggaaagcggc ccccagaacc 150

gaccacaccg tggcaagagg acccagaacc cgaggacgaa aacttgtatg 200

agaagaaccc agactcccat ggttatgaca aggaccccgt tttggacgtc 250

tggaacatgc gacttgtctt cttctttggc gtctccatca tcctggtcct 300

tggcagcacc tttgtggcct atctgcctga ctacaggatg aaagagtggt 350

cccgccgcga agctgagagg cttgtgaaat accgagaggc caatggcctt 400

cccatcatgg aatccaactg cttcgacccc agcaagatcc ag 442

<210> 336
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 336
ctgagaccct gcagcaccat ctg 23

<210> 337
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 337
ggtgcttctt gagccccact tagc 24

<210> 338
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 338
aatctagctt ctccaggact gtggtcgccc cgtccgctgt 40

<210> 339
<211> 2162
<212> DNA

<213> Homo sapiens

<400> 339
gcggcggcta tgccgcttgc tctgctcgtc ctgttgctcc tggggcccgg 50

cggctggtgc cttgcagaac ccccacgcga cagcctgcgg gaggaacttg 100

tcatcacccc gctgccttcc ggggacgtag ccgccacatt ccagttccgc 150

acgcgctggg attcggagct tcagcgggaa ggagtgtccc attacaggct 200

ctttcccaaa gccctggggc agctgatctc caagtattct ctacgggagc 250

tgcacctgtc attcacacaa ggcttttgga ggacccgata ctgggggcca 300

cccttcctgc aggccccatc aggtgcagag ctgtgggtct ggttccaaga 350

cactgtcact gatgtggata aatcttggaa ggagctcagt aatgtcctct 400

cagggatctt ctgcgcctct ctcaacttca tcgactccac caacacagtc 450

actcccactg cctccttcaa acccctgggt ctggccaatg acactgacca 500

ctactttctg cgctatgctg tgctgccgcg ggaggtggtc tgcaccgaaa 550

acctcacccc ctggaagaag ctcttgccct gtagttccaa ggcaggcctc 600

tctgtgctgc tgaaggcaga tcgcttgttc cacaccagct accactccca 650

ggcagtgcat atccgccctg tttgcagaaa tgcacgctgt actagcatct 700

cctgggagct gaggcagacc ctgtcagttg tatttgatgc cttcatcacg 750

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cacggagccc tgccccctgg cttcagagag ccgagtctat gtggacatca 850

ccacctacaa ccaggacaac gagacattag aggtgcaccc acccccgacc 900

actacatatc aggacgtcat cctaggcact cggaagacct atgccatcta 950

tgacttgctt gacaccgcca tgatcaacaa ctctcgaaac ctcaacatcc 1000

agctcaagtg gaagagaccc ccagagaatg aggccccccc agtgcccttc 1050

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gagcacactg ctgtacaaca cccacccata ccgggccttc ccggtgctgc 1150

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atcacctcca agggcaagga gaacaaacca agttacatcc actaccagcc 1250

tgcccaggac cggctgcaac cccacctcct ggagatgctg attcagctgc 1300

cggccaactc agtcaccaag gtttccatcc agtttgagcg ggcgctgctg 1350

aagtggaccg agtacacgcc agatcctaac catggcttct atgtcagccc 1400

atctgtcctc agcgcccttg tgcccagcat ggtagcagcc aagccagtgg 1450

actgggaaga gagtcccctc ttcaacagcc tgttcccagt ctctgatggc 1500

tctaactact ttgtgcggct ctacacggag ccgctgctgg tgaacctgcc 1550

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cacatcgagg agccccgcac aggtggcctg gccaagcggc tggccaacct 1700

tatccggcgc gcccgaggtg tccccccact ctgattcttg ccctttccag 1750

cagctgcagc tgccgtttct ctctggggag gggagcccaa gggctgtttc 1800

tgccacttgc tctcctcaga gttggctttt gaaccaaagt gccctggacc 1850

aggtcagggc ctacagctgt gttgtccagt acaggagcca cgagccaaat 1900

gtggcatttg aatttgaatt aacttagaaa ttcatttcct cacctgtagt 1950

ggccacctct atattgaggt gctcaataag caaaagtggt cggtggctgc 2000

tgtattggac agcacagaaa aagatttcca tcaccacaga aaggtcggct 2050

ggcagcactg gccaaggtga tggggtgtgc tacacagtgt atgtcactgt 2100

gtagtggatg gagtttactg tttgtggaat aaaaacggct gtttccgtgg 2150

aaaaaaaaaa aa 2162

<210> 340
<211> 574
<212> PRT
<213> Homo sapiens

<400> 340

Met	Pro	Leu	Ala	Leu	Leu	Val	Leu	Leu	Leu	Leu	Gly	Pro	Gly	Gly	
1				5				10						15	
Trp	Cys	Leu	Ala	Glu	Pro	Pro	Arg	Asp	Ser	Leu	Arg	Glu	Glu	Leu	
				20				25						30	
Val	Ile	Thr	Pro	Leu	Pro	Ser	Gly	Asp	Val	Ala	Ala	Thr	Phe	Gln	
				35				40						45	
Phe	Arg	Thr	Arg	Trp	Asp	Ser	Glu	Leu	Gln	Arg	Glu	Gly	Val	Ser	
				50				55						60	
His	Tyr	Arg	Leu	Phe	Pro	Lys	Ala	Leu	Gly	Gln	Leu	Ile	Ser	Lys	
				65				70						75	
Tyr	Ser	Leu	Arg	Glu	Leu	His	Leu	Ser	Phe	Thr	Gln	Gly	Phe	Trp	
				80				85						90	
Arg	Thr	Arg	Tyr	Trp	Gly	Pro	Pro	Phe	Leu	Gln	Ala	Pro	Ser	Gly	
				95				100						105	
Ala	Glu	Leu	Trp	Val	Trp	Phe	Gln	Asp	Thr	Val	Thr	Asp	Val	Asp	
				110				115						120	
Lys	Ser	Trp	Lys	Glu	Leu	Ser	Asn	Val	Leu	Ser	Gly	Ile	Phe	Cys	
				125				130						135	
Ala	Ser	Leu	Asn	Phe	Ile	Asp	Ser	Thr	Asn	Thr	Val	Thr	Pro	Thr	
				140				145						150	

Ala Ser Phe Lys Pro Leu Gly Leu Ala Asn Asp Thr Asp His Tyr
155 160 165

Phe Leu Arg Tyr Ala Val Leu Pro Arg Glu Val Val Cys Thr Glu
170 175 180

Asn Leu Thr Pro Trp Lys Lys Leu Leu Pro Cys Ser Ser Lys Ala
185 190 195

Gly Leu Ser Val Leu Leu Lys Ala Asp Arg Leu Phe His Thr Ser
200 205 210

Tyr His Ser Gln Ala Val His Ile Arg Pro Val Cys Arg Asn Ala
215 220 225

Arg Cys Thr Ser Ile Ser Trp Glu Leu Arg Gln Thr Leu Ser Val
230 235 240

Val Phe Asp Ala Phe Ile Thr Gly Gln Gly Lys Lys Asp Trp Ser
245 250 255

Leu Phe Arg Met Phe Ser Arg Thr Leu Thr Glu Pro Cys Pro Leu
260 265 270

Ala Ser Glu Ser Arg Val Tyr Val Asp Ile Thr Thr Tyr Asn Gln
275 280 285

Asp Asn Glu Thr Leu Glu Val His Pro Pro Pro Thr Thr Thr Tyr
290 295 300

Gln Asp Val Ile Leu Gly Thr Arg Lys Thr Tyr Ala Ile Tyr Asp
305 310 315

Leu Leu Asp Thr Ala Met Ile Asn Asn Ser Arg Asn Leu Asn Ile
320 325 330

Gln Leu Lys Trp Lys Arg Pro Pro Glu Asn Glu Ala Pro Pro Val
335 340 345

Pro Phe Leu His Ala Gln Arg Tyr Val Ser Gly Tyr Gly Leu Gln
350 355 360

Lys Gly Glu Leu Ser Thr Leu Leu Tyr Asn Thr His Pro Tyr Arg
365 370 375

Ala Phe Pro Val Leu Leu Leu Asp Thr Val Pro Trp Tyr Leu Arg
380 385 390

Leu Tyr Val His Thr Leu Thr Ile Thr Ser Lys Gly Lys Glu Asn
395 400 405

Lys Pro Ser Tyr Ile His Tyr Gln Pro Ala Gln Asp Arg Leu Gln
410 415 420

Pro His Leu Leu Glu Met Leu Ile Gln Leu Pro Ala Asn Ser Val
425 430 435

Thr Lys Val Ser Ile Gln Phe Glu Arg Ala Leu Leu Lys Trp Thr
440 445 450

Glu Tyr Thr Pro Asp Pro Asn His Gly Phe Tyr Val Ser Pro Ser
455 460 465

Val Leu Ser Ala Leu Val Pro Ser Met Val Ala Ala Lys Pro Val
470 475 480

Asp Trp Glu Glu Ser Pro Leu Phe Asn Ser Leu Phe Pro Val Ser
485 490 495

Asp Gly Ser Asn Tyr Phe Val Arg Leu Tyr Thr Glu Pro Leu Leu
500 505 510

Val Asn Leu Pro Thr Pro Asp Phe Ser Met Pro Tyr Asn Val Ile
515 520 525

Cys Leu Thr Cys Thr Val Val Ala Val Cys Tyr Gly Ser Phe Tyr
530 535 540

Asn Leu Leu Thr Arg Thr Phe His Ile Glu Glu Pro Arg Thr Gly
545 550 555

Gly Leu Ala Lys Arg Leu Ala Asn Leu Ile Arg Arg Ala Arg Gly
560 565 570

Val Pro Pro Leu

<210> 341
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 341
tggacaccgt accctggtat ctgc 24

<210> 342
<211> 24
<212> DNA
<213> Artificial Seqeunce

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic oligonucleotide probe

<400> 342
ccaactctga ggagagcaag tggc 24

<210> 343
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 343
tgtatgtgca caccctcacc atcacctcca agggcaagga gaac 44

<210> 344
<211> 762
<212> DNA
<213> Homo sapiens

<400> 344
caacatgggg tccagcagct tcttggtcct catggtgtct ctcgttcttg 50

tgaccctggt ggctgtggaa ggagttaaag agggtataga gaaagcaggg 100

gtttgcccag ctgacaacgt acgctgcttc aagtccgatc ctccccagtg 150

tcacacagac caggactgtc tgggggaaag gaagtgttgt tacctgcact 200

gtggcttcaa gtgtgtgatt cctgtgaagg aactggaaga aggaggaaac 250

aaggatgaag atgtgtcaag gccataccct gagccaggat gggaggccaa 300

gtgtccaggc tcctcctcta ccaggtgtcc tcagaaatga tgctgggtcc 350

tttctacctc tgggggtcac tctcacttgg cacctgcccc tgagggtcct 400

gagacttgga atatggaaga agcaataccc aaccccacca aagaaaacct 450

gagcttgaag tccttttccc caaaaagagg gaagagtcac aaaaagtcca 500

gaccccaggg acggtacttt ccctctctac ctggtgctcc tccctaatgc 550

tcatgaatgg acccctcatg aatgaaacca gtgcccttat aagagacccc 600

aaagagctgc cttgcccttc tgcaatgtgt gatcacagct agaaggcact 650

gtcagagaag agaaactggt cctcaccaga tgctgaatct gctggtgcct 700

tgatcttgga cttcccagcc tctagaactg taagaaataa atatttgctg 750

tttataatcc aa 762

<210> 345
<211> 111
<212> PRT
<213> Homo sapiens

<400> 345
Met Gly Ser Ser Ser Phe Leu Val Leu Met Val Ser Leu Val Leu
1 5 10 15

Val Thr Leu Val Ala Val Glu Gly Val Lys Glu Gly Ile Glu Lys
20 25 30

Ala Gly Val Cys Pro Ala Asp Asn Val Arg Cys Phe Lys Ser Asp
35 40 45

Pro Pro Gln Cys His Thr Asp Gln Asp Cys Leu Gly Glu Arg Lys
50 55 60

Cys Cys Tyr Leu His Cys Gly Phe Lys Cys Val Ile Pro Val Lys
65 70 75

Glu Leu Glu Glu Gly Gly Asn Lys Asp Glu Asp Val Ser Arg Pro
80 85 90

Tyr Pro Glu Pro Gly Trp Glu Ala Lys Cys Pro Gly Ser Ser Ser
95 100 105

Thr Arg Cys Pro Gln Lys
110

<210> 346
<211> 2528
<212> DNA
<213> Homo sapiens

<400> 346
aaactcagca cttgccggag tggctcattg ttaagacaaa gggtgtgcac 50

ttcctggcca ggaaacctga gcggtgagac tcccagctgc ctacatcaag 100

gccccaggac atgcagaacc ttcctctaga acccgaccca ccaccatgag 150

gtcctgcctg tggagatgca ggcacctgag ccaaggcgtc cagtggtcct 200

tgcttctggc tgtcctggtc ttctttctct tcgccttgcc ctcttttatt 250

aaggagcctc aaacaaagcc ttccaggcat caacgcacag agaacattaa 300

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gggcgaggag gacaaccatc tatgcagagc cagcgccaga gaacaatgcc 400

ctcaacacac aaacccagcc caaggcccac accaccggag acagaggaaa 450

ggaggccaac caggcaccgc cggaggagca ggacaaggtg ccccacacag 500

cacagagggc agcatggaag agcccagaaa aagagaaaac catggtgaac 550

acactgtcac ccagagggca agatgcaggg atggcctctg gcaggacaga 600

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ggcaaagcgg caaccacagc caagacgctc attcccaaaa gtcagcacag 750

aatgctggct cccacaggag cagtgtcaac aaggacgaga cagaaaggag 800

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gcaacggggg catcctgaac aactcccaca tgggccagga gatagacagt 1300

cacgactacg tgttccgatt gagcggagct ctcattaaag gctacgaaca 1350

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cccagtcact ccttatattg ggcaatcggg gtttcaagaa cgtgcctctt 1450

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gtggctggaa gcactgctta tgaatcagac ggtgatgtca aaaaaccttt 1550

tctggttcag gcacagaccc caggaagctt ttcgggaagc cctgcacatg 1600

gacaggtacc tgttgctgca cccagacttt ctccgataca tgaagaacag 1650

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cggctgtacc agcgtcctgg tcccggaact gccaaagcca agaactgacc 1950

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ctgtaggtcc tgaggccagg gatttttaat taaatggggt gatgggtggc 2200

caataccaca attcctgctg aaaaacactc ttccagtcca aaagcttctt 2250

gatacagaaa aaagagcctg gatttacaga aacatataga tctggtttga 2300

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ggtctatact tgtccttgtc tttaagctat ttgacaactc tacgtgttgt 2450

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<210> 347
<211> 600
<212> PRT
<213> Homo sapiens

<400> 347

Met	Arg	Ser	Cys	Leu	Trp	Arg	Cys	Arg	His	Leu	Ser	Gln	Gly	Val	
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Gln	Trp	Ser	Leu	Leu	Leu	Ala	Val	Leu	Val	Phe	Phe	Leu	Phe	Ala	
				20				25						30	
Leu	Pro	Ser	Phe	Ile	Lys	Glu	Pro	Gln	Thr	Lys	Pro	Ser	Arg	His	
				35				40						45	
Gln	Arg	Thr	Glu	Asn	Ile	Lys	Glu	Arg	Ser	Leu	Gln	Ser	Leu	Ala	
				50				55						60	

Lys Pro Lys Ser Gln Ala Pro Thr Arg Ala Arg Arg Thr Thr Ile

65 70 75

Tyr Ala Glu Pro Ala Pro Glu Asn Asn Ala Leu Asn Thr Gln Thr
80 85 90

Gln Pro Lys Ala His Thr Thr Gly Asp Arg Gly Lys Glu Ala Asn
95 100 105

Gln Ala Pro Pro Glu Glu Gln Asp Lys Val Pro His Thr Ala Gln
110 115 120

Arg Ala Ala Trp Lys Ser Pro Glu Lys Glu Lys Thr Met Val Asn
125 130 135

Thr Leu Ser Pro Arg Gly Gln Asp Ala Gly Met Ala Ser Gly Arg
140 145 150

Thr Glu Ala Gln Ser Trp Lys Ser Gln Asp Thr Lys Thr Thr Gln
155 160 165

Gly Asn Gly Gly Gln Thr Arg Lys Leu Thr Ala Ser Arg Thr Val
170 175 180

Ser Glu Lys His Gln Gly Lys Ala Ala Thr Thr Ala Lys Thr Leu
185 190 195

Ile Pro Lys Ser Gln His Arg Met Leu Ala Pro Thr Gly Ala Val
200 205 210

Ser Thr Arg Thr Arg Gln Lys Gly Val Thr Thr Ala Val Ile Pro
215 220 225

Pro Lys Glu Lys Lys Pro Gln Ala Thr Pro Pro Pro Ala Pro Phe
230 235 240

Gln Ser Pro Thr Thr Gln Arg Asn Gln Arg Leu Lys Ala Ala Asn
245 250 255

Phe Lys Ser Glu Pro Arg Trp Asp Phe Glu Glu Lys Tyr Ser Phe
260 265 270

Glu Ile Gly Gly Leu Gln Thr Thr Cys Pro Asp Ser Val Lys Ile
275 280 285

Lys Ala Ser Lys Ser Leu Trp Leu Gln Lys Leu Phe Leu Pro Asn
290 295 300

Leu Thr Leu Phe Leu Asp Ser Arg His Phe Asn Gln Ser Glu Trp
305 310 315

Asp Arg Leu Glu His Phe Ala Pro Pro Phe Gly Phe Met Glu Leu
320 325 330

Asn Tyr Ser Leu Val Gln Lys Val Val Thr Arg Phe Pro Pro Val
335 340 345

Pro Gln Gln Gln Leu Leu Leu Ala Ser Leu Pro Ala Gly Ser Leu
350 355 360

Arg Cys Ile Thr Cys Ala Val Val Gly Asn Gly Gly Ile Leu Asn
365 370 375

Asn Ser His Met Gly Gln Glu Ile Asp Ser His Asp Tyr Val Phe

380 385 390

Arg Leu Ser Gly Ala Leu Ile Lys Gly Tyr Glu Gln Asp Val Gly
395 400 405

Thr Arg Thr Ser Phe Tyr Gly Phe Thr Ala Phe Ser Leu Thr Gln
410 415 420

Ser Leu Leu Ile Leu Gly Asn Arg Gly Phe Lys Asn Val Pro Leu
425 430 435

Gly Lys Asp Val Arg Tyr Leu His Phe Leu Glu Gly Thr Arg Asp
440 445 450

Tyr Glu Trp Leu Glu Ala Leu Leu Met Asn Gln Thr Val Met Ser
455 460 465

Lys Asn Leu Phe Trp Phe Arg His Arg Pro Gln Glu Ala Phe Arg
470 475 480

Glu Ala Leu His Met Asp Arg Tyr Leu Leu Leu His Pro Asp Phe
485 490 495

Leu Arg Tyr Met Lys Asn Arg Phe Leu Arg Ser Lys Thr Leu Asp
500 505 510

Gly Ala His Trp Arg Ile Tyr Arg Pro Thr Thr Gly Ala Leu Leu
515 520 525

Leu Leu Thr Ala Leu Gln Leu Cys Asp Gln Val Ser Ala Tyr Gly
530 535 540

Phe Ile Thr Glu Gly His Glu Arg Phe Ser Asp His Tyr Tyr Asp
545 550 555

Thr Ser Trp Lys Arg Leu Ile Phe Tyr Ile Asn His Asp Phe Lys
560 565 570

Leu Glu Arg Glu Val Trp Lys Arg Leu His Asp Glu Gly Ile Ile
575 580 585

Arg Leu Tyr Gln Arg Pro Gly Pro Gly Thr Ala Lys Ala Lys Asn
590 595 600

<210> 348
<211> 496
<212> DNA
<213> Homo sapiens

<400> 348
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gggccttcgc cggagcagcg agtggaaatt gttcctcgag atctgaggat 100

gaaggacaag tttctaaaac accttacagg ccctctttat tttagtccaa 150

agtgcagcaa acacttccat agactttatc acaacaccag agactgcacc 200

attcctgcat actataaaag atgcgccagg cttcttaccc ggctggctgt 250

cagtccagtg tgcatggagg ataagtgagc agaccgtaca ggagcagcac 300

accaggagcc atgagaagtg ccttggaaac caacagggaa acagaactat 350

ctttatacac atcccctcat ggacaagaga tttatttttg cagacagact 400

cttccataag tcctttgagt tttgtatgtt gttgacagtt tgcagatata 450

tattcgataa atcagtgtac ttgacagtgt tatctgtcac ttattt 496

<210> 349
<211> 91
<212> PRT
<213> Homo sapiens

<400> 349

Met	Arg	Gly	Pro	Gly	His	Pro	Leu	Leu	Leu	Gly	Leu	Leu	Leu	Val	
1				5				10						15	
Leu	Gly	Pro	Ser	Pro	Glu	Gln	Arg	Val	Glu	Ile	Val	Pro	Arg	Asp	
			20					25						30	
Leu	Arg	Met	Lys	Asp	Lys	Phe	Leu	Lys	His	Leu	Thr	Gly	Pro	Leu	
			35					40						45	
Tyr	Phe	Ser	Pro	Lys	Cys	Ser	Lys	His	Phe	His	Arg	Leu	Tyr	His	
			50					55						60	
Asn	Thr	Arg	Asp	Cys	Thr	Ile	Pro	Ala	Tyr	Tyr	Lys	Arg	Cys	Ala	
			65					70						75	
Arg	Leu	Leu	Thr	Arg	Leu	Ala	Val	Ser	Pro	Val	Cys	Met	Glu	Asp	
			80					85						90	

Lys

<210> 350
<211> 1141
<212> DNA
<213> Homo sapiens

<400> 350
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ttctctggga ggcccgaccc cggccgcgcc cagcccccac catgccaccc 100

gcggggctcc gccgggccgc gccgctcacc gcaatcgctc tgttggtgct 150

gggggctccc ctggtgctgg ccggcgagga ctgcctgtgg tacctggacc 200

ggaatggctc ctggcatccg gggtttaact gcgagttctt caccttctgc 250

tgcgggacct gctaccatcg gtactgctgc agggacctga ccttgcttat 300

caccgagagg cagcagaagc actgcctggc cttcagcccc aagaccatag 350

caggcatcgc ctcagctgtg atcctctttg ttgctgtggt tgccaccacc 400

atctgctgct tcctctgttc ctgttgctac ctgtaccgcc ggcgccagca 450

gctccagagc ccatttgaag gccaggagat tccaatgaca ggcatcccag 500

tgcagccagt atacccatac ccccaggacc ccaaagctgg ccctgcaccc 550

ccacagcctg gcttcatgta cccacctagt ggtcctgctc cccaatatcc 600

actctaccca gctgggcccc cagtctacaa ccctgcagct cctcctccct 650

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tctgctgccc cttcagtgat gccaaccttg ggagatgccc tcatcctgta 750

cctgcatctg gtcctggggg tggcaggagt cctccagcca ccaggcccca 800

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aacaggagct gaactagaac tatgaggggt tgggggggagg gcttggaatt 900

atgggctatt tttactgggg gcaagggagg gagatgacag cctgggtcac 950

agtgcctgtt ttcaaatagt ccctctgctc ccaagatccc agccaggaag 1000

gctggggccc tactgtttgt cccctctggg ctggggtggg gggagggagg 1050

aggttccgtc agcagctggc agtagccctc ctctctggct gccccactgg 1100

ccacatctct ggcctgctag attaaagctg taaagacaaa a 1141

<210> 351
<211> 197
<212> PRT
<213> Homo sapiens

<400> 351

Met	Pro	Pro	Ala	Gly	Leu	Arg	Arg	Ala	Ala	Pro	Leu	Thr	Ala	Ile					
1					5					10					15				
Ala	Leu	Leu	Val	Leu	Gly	Ala	Pro	Leu	Val	Leu	Ala	Gly	Glu	Asp					
				20					25					30					
Cys	Leu	Trp	Tyr	Leu	Asp	Arg	Asn	Gly	Ser	Trp	His	Pro	Gly	Phe					
				35					40					45					
Asn	Cys	Glu	Phe	Phe	Thr	Phe	Cys	Cys	Gly	Thr	Cys	Tyr	His	Arg					
				50					55					60					
Tyr	Cys	Cys	Arg	Asp	Leu	Thr	Leu	Leu	Ile	Thr	Glu	Arg	Gln	Gln					
				65					70					75					
Lys	His	Cys	Leu	Ala	Phe	Ser	Pro	Lys	Thr	Ile	Ala	Gly	Ile	Ala					
				80					85					90					
Ser	Ala	Val	Ile	Leu	Phe	Val	Ala	Val	Val	Ala	Thr	Thr	Ile	Cys					
				95					100					105					
Cys	Phe	Leu	Cys	Ser	Cys	Cys	Tyr	Leu	Tyr	Arg	Arg	Arg	Gln	Gln					
				110					115					120					
Leu	Gln	Ser	Pro	Phe	Glu	Gly	Gln	Glu	Ile	Pro	Met	Thr	Gly	Ile					
				125					130					135					
Pro	Val	Gln	Pro	Val	Tyr	Pro	Tyr	Pro	Gln	Asp	Pro	Lys	Ala	Gly					
				140					145					150					
Pro	Ala	Pro	Pro	Gln	Pro	Gly	Phe	Met	Tyr	Pro	Pro	Ser	Gly	Pro					
				155					160					165					
Ala	Pro	Gln	Tyr	Pro	Leu	Tyr	Pro	Ala	Gly	Pro	Pro	Val	Tyr	Asn					
				170					175					180					

Pro Ala Ala Pro Pro Pro Tyr Met Pro Pro Gln Pro Ser Tyr Pro
185 190 195

Gly Ala

<210> 352
<211> 3226
<212> DNA
<213> Homo sapiens

<400> 352
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gcggccccag aaccccaggt aggtagagca agaagatggt gtttctgccc 100

ctcaaatggt cccttgcaac catgtcattt ctactttcct cactgttggc 150

tctcttaact gtgtccactc cttcatggtg tcagagcact gaagcatctc 200

caaaacgtag tgatgggaca ccatttcctt ggaataaaat acgacttcct 250

gagtacgtca tcccagttca ttatgatctc ttgatccatg caaaccttac 300

cacgctgacc ttctggggaa ccacgaaagt agaaatcaca gccagtcagc 350

ccaccagcac catcatcctg catagtcacc acctgcagat atctagggcc 400

accctcagga agggagctgg agagaggcta tcggaagaac ccctgcaggt 450

cctggaacac ccccctcagg agcaaattgc actgctggct cccgagcccc 500

tccttgtcgg gctcccgtac acagttgtca ttcactatgc tggcaatctt 550

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ggaactgagg atactagcat caacacaatt tgaacccact gcagctagaa 650

tggcctttcc ctgctttgat gaacctgcct tcaaagcaag tttctcaatc 700

aaaattagaa gagagccaag gcacctagcc atctccaata tgccattggt 750

gaaatctgtg actgttgctg aaggactcat agaagaccat tttgatgtca 800

ctgtgaagat gagcacctat ctggtggcct tcatcatttc agattttgag 850

tctgtcagca agataaccaa gagtggagtc aaggtttctg tttatgctgt 900

gccagacaag ataaatcaag cagattatgc actggatgct gcggtgactc 950

ttctagaatt ttatgaggat tatttcagca taccgtatcc cctacccaaa 1000

caagatcttg ctgctattcc cgactttcag tctggtgcta tggaaaactg 1050

gggactgaca acatatagag aatctgctct gttgtttgat gcagaaaagt 1100

cttctgcatc aagtaagctt ggcatcacag tgactgtggc ccatgaactg 1150

gcccaccagt ggtttgggaa cctggtcact atggaatggt ggaatgatct 1200

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tgtggaaaat cctgctcaga tccgggagat gtttgatgat gtttcttatg 1400

ataagggagc ttgtattctg aatatgctaa gggagtatct tagcgctgac 1450

gcatttaaaa gtggtattgt acagtatctc cagaagcata gctataaaaa 1500

tacaaaaaac gaggacctgt gggatagtat ggcaagtatt tgccctacag 1550

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tcatcctcac attggcatca ggaaggggtg gatgtgaaaa ccatgatgaa 1650

cacttggaca ctgcagaggg gttttcccct aataaccatc acagtgaggg 1700

ggaggaatgt acacatgaag caagagcact acatgaaggg ctctgacggc 1750

gccccggaca ctgggtacct gtggcatgtt ccattgacat tcatcaccag 1800

caaatccaac atggtccatc gatttttgct aaaaacaaaa acagatgtgc 1850

tcatcctccc agaagaggtg gaatggatca aatttaatgt gggcatgaat 1900

ggctattaca ttgtgcatta cgaggatgat ggatgggact ctttgactgg 1950

ccttttaaaa ggaacacaca cagcagtcag cagtaatgat cgggcaagtc 2000

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cgtgtttcaa ggtttgaatg agctgattcc tatgtataag ttaatggaga 2150

aaagagatat gaatgaagtg gaaactcaat tcaaggcctt cctcatcagg 2200

ctgctaaggg acctcattga taagcagaca tggacagacg agggctcagt 2250

ctcagagcaa atgctgcgga gtgaactact actcctcgcc tgtgtgcaca 2300

actatcagcc gtgcgtacag agggcagaag gctatttcag aaagtggaag 2350

gaatccaatg gaaacttgag cctgcctgtc gacgtgacct tggcagtgtt 2400

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atcagttttc tttgtccagt actgagaaaa gccaaattga atttgccctc 2500

tgcagaaccc aaaataagga aaagcttcaa tggctactag atgaaagctt 2550

taagggagat aaaataaaaa ctcaggagtt tccacaaatt cttacactca 2600

ttggcaggaa cccagtagga tacccactgg cctggcaatt tctgaggaaa 2650

aactggaaca aacttgtaca aaagtttgaa cttggctcat cttccatagc 2700

ccacatggta atgggtacaa caaatcaatt ctccacaaga acacggcttg 2750

aagaggtaaa aggattcttc agctctttga aagaaaatgg ttctcagctc 2800

cgttgtgtcc aacagacaat tgaaaccatt gaagaaaaca tcggttggat 2850

ggataagaat tttgataaaa tcagagtgtg gctgcaaagt gaaaagcttg 2900

aacgtatgta aaaattcctc ccttgcccgg ttcctgttat ctctaatcac 2950

caacattttg ttgagtgtat tttcaaacta gagatggctg ttttggctcc 3000

aactggagat actttttttcc cttcaactca ttttttgact atccctgtga 3050

aaagaatagc tgttagtttt tcatgaatgg gctttttcat gaatgggcta 3100

tcgctaccat gtgttttgtt catcacaggt gttgccctgc aacgtaaacc 3150

caagtgttgg gttccctgcc acagaagaat aaagtacctt attcttctca 3200

aaaaaaaaaa aaaaaaaaaa aaaaaa 3226

<210> 353
<211> 941
<212> PRT
<213> Homo sapiens

<400> 353

Met	Val	Phe	Leu	Pro	Leu	Lys	Trp	Ser	Leu	Ala	Thr	Met	Ser	Phe	
1				5				10						15	
Leu	Leu	Ser	Ser	Leu	Leu	Ala	Leu	Leu	Thr	Val	Ser	Thr	Pro	Ser	
				20				25						30	
Trp	Cys	Gln	Ser	Thr	Glu	Ala	Ser	Pro	Lys	Arg	Ser	Asp	Gly	Thr	
				35				40						45	
Pro	Phe	Pro	Trp	Asn	Lys	Ile	Arg	Leu	Pro	Glu	Tyr	Val	Ile	Pro	
				50				55						60	
Val	His	Tyr	Asp	Leu	Leu	Ile	His	Ala	Asn	Leu	Thr	Thr	Leu	Thr	
				65				70						75	
Phe	Trp	Gly	Thr	Thr	Lys	Val	Glu	Ile	Thr	Ala	Ser	Gln	Pro	Thr	
				80				85						90	
Ser	Thr	Ile	Ile	Leu	His	Ser	His	His	Leu	Gln	Ile	Ser	Arg	Ala	
				95				100						105	
Thr	Leu	Arg	Lys	Gly	Ala	Gly	Glu	Arg	Leu	Ser	Glu	Glu	Pro	Leu	
				110				115						120	
Gln	Val	Leu	Glu	His	Pro	Pro	Gln	Glu	Gln	Ile	Ala	Leu	Leu	Ala	
				125				130						135	
Pro	Glu	Pro	Leu	Leu	Val	Gly	Leu	Pro	Tyr	Thr	Val	Val	Ile	His	
				140				145						150	
Tyr	Ala	Gly	Asn	Leu	Ser	Glu	Thr	Phe	His	Gly	Phe	Tyr	Lys	Ser	
				155				160						165	
Thr	Tyr	Arg	Thr	Lys	Glu	Gly	Glu	Leu	Arg	Ile	Leu	Ala	Ser	Thr	
				170				175						180	
Gln	Phe	Glu	Pro	Thr	Ala	Ala	Arg	Met	Ala	Phe	Pro	Cys	Phe	Asp	
				185				190						195	
Glu	Pro	Ala	Phe	Lys	Ala	Ser	Phe	Ser	Ile	Lys	Ile	Arg	Arg	Glu	
				200				205						210	
Pro	Arg	His	Leu	Ala	Ile	Ser	Asn	Met	Pro	Leu	Val	Lys	Ser	Val	

215 220 225

Thr Val Ala Glu Gly Leu Ile Glu Asp His Phe Asp Val Thr Val
230 235 240

Lys Met Ser Thr Tyr Leu Val Ala Phe Ile Ile Ser Asp Phe Glu
245 250 255

Ser Val Ser Lys Ile Thr Lys Ser Gly Val Lys Val Ser Val Tyr
260 265 270

Ala Val Pro Asp Lys Ile Asn Gln Ala Asp Tyr Ala Leu Asp Ala
275 280 285

Ala Val Thr Leu Leu Glu Phe Tyr Glu Asp Tyr Phe Ser Ile Pro
290 295 300

Tyr Pro Leu Pro Lys Gln Asp Leu Ala Ala Ile Pro Asp Phe Gln
305 310 315

Ser Gly Ala Met Glu Asn Trp Gly Leu Thr Thr Tyr Arg Glu Ser
320 325 330

Ala Leu Leu Phe Asp Ala Glu Lys Ser Ser Ala Ser Ser Lys Leu
335 340 345

Gly Ile Thr Val Thr Val Ala His Glu Leu Ala His Gln Trp Phe
350 355 360

Gly Asn Leu Val Thr Met Glu Trp Trp Asn Asp Leu Trp Leu Asn
365 370 375

Glu Gly Phe Ala Lys Phe Met Glu Phe Val Ser Val Ser Val Thr
380 385 390

His Pro Glu Leu Lys Val Gly Asp Tyr Phe Phe Gly Lys Cys Phe
395 400 405

Asp Ala Met Glu Val Asp Ala Leu Asn Ser Ser His Pro Val Ser
410 415 420

Thr Pro Val Glu Asn Pro Ala Gln Ile Arg Glu Met Phe Asp Asp
425 430 435

Val Ser Tyr Asp Lys Gly Ala Cys Ile Leu Asn Met Leu Arg Glu
440 445 450

Tyr Leu Ser Ala Asp Ala Phe Lys Ser Gly Ile Val Gln Tyr Leu
455 460 465

Gln Lys His Ser Tyr Lys Asn Thr Lys Asn Glu Asp Leu Trp Asp
470 475 480

Ser Met Ala Ser Ile Cys Pro Thr Asp Gly Val Lys Gly Met Asp
485 490 495

Gly Phe Cys Ser Arg Ser Gln His Ser Ser Ser Ser Ser His Trp
500 505 510

His Gln Glu Gly Val Asp Val Lys Thr Met Met Asn Thr Trp Thr
515 520 525

Leu Gln Arg Gly Phe Pro Leu Ile Thr Ile Thr Val Arg Gly Arg

530 535 540

Asn Val His Met Lys Gln Glu His Tyr Met Lys Gly Ser Asp Gly
545 550 555

Ala Pro Asp Thr Gly Tyr Leu Trp His Val Pro Leu Thr Phe Ile
560 565 570

Thr Ser Lys Ser Asn Met Val His Arg Phe Leu Leu Lys Thr Lys
575 580 585

Thr Asp Val Leu Ile Leu Pro Glu Glu Val Glu Trp Ile Lys Phe
590 595 600

Asn Val Gly Met Asn Gly Tyr Tyr Ile Val His Tyr Glu Asp Asp
605 610 615

Gly Trp Asp Ser Leu Thr Gly Leu Leu Lys Gly Thr His Thr Ala
620 625 630

Val Ser Ser Asn Asp Arg Ala Ser Leu Ile Asn Asn Ala Phe Gln
635 640 645

Leu Val Ser Ile Gly Lys Leu Ser Ile Glu Lys Ala Leu Asp Leu
650 655 660

Ser Leu Tyr Leu Lys His Glu Thr Glu Ile Met Pro Val Phe Gln
665 670 675

Gly Leu Asn Glu Leu Ile Pro Met Tyr Lys Leu Met Glu Lys Arg
680 685 690

Asp Met Asn Glu Val Glu Thr Gln Phe Lys Ala Phe Leu Ile Arg
695 700 705

Leu Leu Arg Asp Leu Ile Asp Lys Gln Thr Trp Thr Asp Glu Gly
710 715 720

Ser Val Ser Glu Gln Met Leu Arg Ser Glu Leu Leu Leu Leu Ala
725 730 735

Cys Val His Asn Tyr Gln Pro Cys Val Gln Arg Ala Glu Gly Tyr
740 745 750

Phe Arg Lys Trp Lys Glu Ser Asn Gly Asn Leu Ser Leu Pro Val
755 760 765

Asp Val Thr Leu Ala Val Phe Ala Val Gly Ala Gln Ser Thr Glu
770 775 780

Gly Trp Asp Phe Leu Tyr Ser Lys Tyr Gln Phe Ser Leu Ser Ser
785 790 795

Thr Glu Lys Ser Gln Ile Glu Phe Ala Leu Cys Arg Thr Gln Asn
800 805 810

Lys Glu Lys Leu Gln Trp Leu Leu Asp Glu Ser Phe Lys Gly Asp
815 820 825

Lys Ile Lys Thr Gln Glu Phe Pro Gln Ile Leu Thr Leu Ile Gly
830 835 840

Arg Asn Pro Val Gly Tyr Pro Leu Ala Trp Gln Phe Leu Arg Lys

845 850 855

Asn Trp Asn Lys Leu Val Gln Lys Phe Glu Leu Gly Ser Ser Ser
860 865 870

Ile Ala His Met Val Met Gly Thr Thr Asn Gln Phe Ser Thr Arg
875 880 885

Thr Arg Leu Glu Glu Val Lys Gly Phe Phe Ser Ser Leu Lys Glu
890 895 900

Asn Gly Ser Gln Leu Arg Cys Val Gln Gln Thr Ile Glu Thr Ile
905 910 915

Glu Glu Asn Ile Gly Trp Met Asp Lys Asn Phe Asp Lys Ile Arg
920 925 930

Val Trp Leu Gln Ser Glu Lys Leu Glu Arg Met
935 940

<210> 354
<211> 1587
<212> DNA
<213> Homo sapiens

<400> 354
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tcatcctccc actgccagga gtgcaggcgc tgctctgcca gtttgggaca 100

gttcagcatg tgtggaaggt gtccgaccta ccccggcaat ggacccctaa 150

gaacaccagc tgcgacagcg gcttggggtg ccaggacacg ttgatgctca 200

ttgagagcgg accccaagtg agcctggtgc tctccaaggg ctgcacggag 250

gccaaggacc aggagccccg cgtcactgag caccggatgg gccccggcct 300

ctccctgatc tcctacacct tcgtgtgccg ccaggaggac ttctgcaaca 350

acctcgttaa ctccctcccg ctttgggccc cacagccccc agcagaccca 400

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gacaacagaa gagatctgcc ccaaggggac cacacactgt tatgatggcc 500

tcctcaggct caggggagga ggcatcttct ccaatctgag agtccaggga 550

tgcatgcccc agccaggttg caacctgctc aatgggacac aggaaattgg 600

gcccgtgggt atgactgaga actgcaatag gaaagatttt ctgacctgtc 650

atcgggggac caccattatg acacacggaa acttggctca agaacccact 700

gattggacca catcgaatac cgagatgtgc gaggtggggc aggtgtgtca 750

ggagacgctg ctgctcatag atgtaggact cacatcaacc ctggtgggga 800

caaaaggctg cagcactgtt ggggctcaaa attcccagaa gaccaccatc 850

cactcagccc ctcctggggt gcttgtggcc tcctataccc acttctgctc 900

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ggctgtccac caaaatgagc attcagggct gcgtggccca accttccagc 1150

ttcttgttga accacaccag acaaatcggg atcttctctg cgcgtgagaa 1200

gcgtgatgtg cagcctcctg cctctcagca tgagggaggt ggggctgagg 1250

gcctggagtc tctcacttgg ggggtggggc tggcactggc cccagcgctg 1300

tggtggggag tggtttgccc ttcctgctaa ctctattacc cccacgattc 1350

ttcaccgctg ctgaccaccc acactcaacc tccctctgac ctcataacct 1400

aatggccttg gacaccagat tctttcccat tctgtccatg aatcatcttc 1450

cccacacaca atcattcata tctactcacc taacagcaac actggggaga 1500

gcctggagca tccggacttg ccctatggga gaggggacgc tggaggagtg 1550

gctgcatgta tctgataata cagaccctgt cctttca 1587

<210> 355
<211> 437
<212> PRT
<213> Homo sapiens

<400> 355

Met	Ser	Ala	Val	Leu	Leu	Leu	Ala	Leu	Leu	Gly	Phe	Ile	Leu	Pro	
1				5				10						15	
Leu	Pro	Gly	Val	Gln	Ala	Leu	Leu	Cys	Gln	Phe	Gly	Thr	Val	Gln	
			20					25						30	
His	Val	Trp	Lys	Val	Ser	Asp	Leu	Pro	Arg	Gln	Trp	Thr	Pro	Lys	
			35					40						45	
Asn	Thr	Ser	Cys	Asp	Ser	Gly	Leu	Gly	Cys	Gln	Asp	Thr	Leu	Met	
			50					55						60	
Leu	Ile	Glu	Ser	Gly	Pro	Gln	Val	Ser	Leu	Val	Leu	Ser	Lys	Gly	
			65					70						75	
Cys	Thr	Glu	Ala	Lys	Asp	Gln	Glu	Pro	Arg	Val	Thr	Glu	His	Arg	
			80					85						90	
Met	Gly	Pro	Gly	Leu	Ser	Leu	Ile	Ser	Tyr	Thr	Phe	Val	Cys	Arg	
			95					100						105	
Gln	Glu	Asp	Phe	Cys	Asn	Asn	Leu	Val	Asn	Ser	Leu	Pro	Leu	Trp	
			110					115						120	
Ala	Pro	Gln	Pro	Pro	Ala	Asp	Pro	Gly	Ser	Leu	Arg	Cys	Pro	Val	
			125					130						135	
Cys	Leu	Ser	Met	Glu	Gly	Cys	Leu	Glu	Gly	Thr	Thr	Glu	Glu	Ile	
			140					145						150	

Cys Pro Lys Gly Thr Thr His Cys Tyr Asp Gly Leu Leu Arg Leu

155 160 165

Arg Gly Gly Gly Ile Phe Ser Asn Leu Arg Val Gln Gly Cys Met
170 175 180

Pro Gln Pro Gly Cys Asn Leu Leu Asn Gly Thr Gln Glu Ile Gly
185 190 195

Pro Val Gly Met Thr Glu Asn Cys Asn Arg Lys Asp Phe Leu Thr
200 205 210

Cys His Arg Gly Thr Thr Ile Met Thr His Gly Asn Leu Ala Gln
215 220 225

Glu Pro Thr Asp Trp Thr Thr Ser Asn Thr Glu Met Cys Glu Val
230 235 240

Gly Gln Val Cys Gln Glu Thr Leu Leu Leu Ile Asp Val Gly Leu
245 250 255

Thr Ser Thr Leu Val Gly Thr Lys Gly Cys Ser Thr Val Gly Ala
260 265 270

Gln Asn Ser Gln Lys Thr Thr Ile His Ser Ala Pro Pro Gly Val
275 280 285

Leu Val Ala Ser Tyr Thr His Phe Cys Ser Ser Asp Leu Cys Asn
290 295 300

Ser Ala Ser Ser Ser Ser Val Leu Leu Asn Ser Leu Pro Pro Gln
305 310 315

Ala Ala Pro Val Pro Gly Asp Arg Gln Cys Pro Thr Cys Val Gln
320 325 330

Pro Leu Gly Thr Cys Ser Ser Gly Ser Pro Arg Met Thr Cys Pro
335 340 345

Arg Gly Ala Thr His Cys Tyr Asp Gly Tyr Ile His Leu Ser Gly
350 355 360

Gly Gly Leu Ser Thr Lys Met Ser Ile Gln Gly Cys Val Ala Gln
365 370 375

Pro Ser Ser Phe Leu Leu Asn His Thr Arg Gln Ile Gly Ile Phe
380 385 390

Ser Ala Arg Glu Lys Arg Asp Val Gln Pro Pro Ala Ser Gln His
395 400 405

Glu Gly Gly Gly Ala Glu Gly Leu Glu Ser Leu Thr Trp Gly Val
410 415 420

Gly Leu Ala Leu Ala Pro Ala Leu Trp Trp Gly Val Val Cys Pro
425 430 435

Ser Cys

<210> 356
<211> 1238
<212> DNA
<213> Homo sapiens

<400> 356
gcgacgggca ggacgccccg ttcgcctagc gcgtgctcag gagttggtgt 50

cctgcctgcg ctcaggatga gggggaatct ggccctggtg ggcgttctaa 100

tcagcctggc cttcctgtca ctgctgccat ctggacatcc tcagccggct 150

ggcgatgacg cctgctctgt gcagatcctc gtccctggcc tcaaagggga 200

tgcgggagag aagggagaca aaggcgcccc cggacggcct ggaagagtcg 250

gccccacggg agaaaaagga gacatggggg acaaaggaca gaaaggcagt 300

gtgggtcgtc atggaaaaat tggtcccatt ggctctaaag gtgagaaagg 350

agattccggt gacataggac cccctggtcc taatggagaa ccaggcctcc 400

catgtgagtg cagccagctg cgcaaggcca tcggggagat ggacaaccag 450

gtctctcagc tgaccagcga gctcaagttc atcaagaatg ctgtcgccgg 500

tgtgcgcgag acggagagca agatctacct gctggtgaag gaggagaagc 550

gctacgcgga cgcccagctg tcctgccagg gccgcggggg cacgctgagc 600

atgcccaagg acgaggctgc caatggcctg atggccgcat acctggcgca 650

agccggcctg gcccgtgtct tcatcggcat caacgacctg gagaaggagg 700

gcgccttcgt gtactctgac cactccccca tgcggacctt caacaagtgg 750

cgcagcggtg agcccaacaa tgcctacgac gaggaggact gcgtggagat 800

ggtggcctcg ggcggctgga acgacgtggc ctgccacacc accatgtact 850

tcatgtgtga gtttgacaag gagaacatgt gagcctcagg ctggggctgc 900

ccattggggg ccccacatgt ccctgcaggg ttggcaggga cagagcccag 950

accatggtgc cagccaggga gctgtccctc tgtgaagggt ggaggctcac 1000

tgagtagagg gctgttgtct aaactgagaa aatggcctat gcttaagagg 1050

aaaatgaaag tgttcctggg gtgctgtctc tgaagaagca gagtttcatt 1100

acctgtattg tagccccaat gtcattatgt aattattacc cagaattgct 1150

cttccataaa gcttgtgcct ttgtccaagc tatacaataa aatctttaag 1200

tagtgcagta gttaagtcca aaaaaaaaaa aaaaaaaa 1238

<210> 357
<211> 271
<212> PRT
<213> Homo sapiens

<400> 357
Met Arg Gly Asn Leu Ala Leu Val Gly Val Leu Ile Ser Leu Ala
1 5 10 15

Phe Leu Ser Leu Leu Pro Ser Gly His Pro Gln Pro Ala Gly Asp
20 25 30

Asp Ala Cys Ser Val Gln Ile Leu Val Pro Gly Leu Lys Gly Asp
35 40 45

Ala Gly Glu Lys Gly Asp Lys Gly Ala Pro Gly Arg Pro Gly Arg
50 55 60

Val Gly Pro Thr Gly Glu Lys Gly Asp Met Gly Asp Lys Gly Gln
65 70 75

Lys Gly Ser Val Gly Arg His Gly Lys Ile Gly Pro Ile Gly Ser
80 85 90

Lys Gly Glu Lys Gly Asp Ser Gly Asp Ile Gly Pro Pro Gly Pro
95 100 105

Asn Gly Glu Pro Gly Leu Pro Cys Glu Cys Ser Gln Leu Arg Lys
110 115 120

Ala Ile Gly Glu Met Asp Asn Gln Val Ser Gln Leu Thr Ser Glu
125 130 135

Leu Lys Phe Ile Lys Asn Ala Val Ala Gly Val Arg Glu Thr Glu
140 145 150

Ser Lys Ile Tyr Leu Leu Val Lys Glu Glu Lys Arg Tyr Ala Asp
155 160 165

Ala Gln Leu Ser Cys Gln Gly Arg Gly Gly Thr Leu Ser Met Pro
170 175 180

Lys Asp Glu Ala Ala Asn Gly Leu Met Ala Ala Tyr Leu Ala Gln
185 190 195

Ala Gly Leu Ala Arg Val Phe Ile Gly Ile Asn Asp Leu Glu Lys
200 205 210

Glu Gly Ala Phe Val Tyr Ser Asp His Ser Pro Met Arg Thr Phe
215 220 225

Asn Lys Trp Arg Ser Gly Glu Pro Asn Asn Ala Tyr Asp Glu Glu
230 235 240

Asp Cys Val Glu Met Val Ala Ser Gly Gly Trp Asn Asp Val Ala
245 250 255

Cys His Thr Thr Met Tyr Phe Met Cys Glu Phe Asp Lys Glu Asn
260 265 270

Met

<210> 358
<211> 972
<212> DNA
<213> Homo sapiens

<400> 358
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gagcaccggc agcaccagtg tgtgagggga gcaggcagcg gtcctagcca 100

gttccttgat cctgccagac cacccagccc ccggcacaga gctgctccac 150

aggcaccatg aggatcatgc tgctattcac agccatcctg gccttcagcc 200

tagctcagag ctttggggct gtctgtaagg agccacagga ggaggtggtt 250

cctggcgggg gccgcagcaa gagggatcca gatctctacc agctgctcca 300

gagactcttc aaaagccact catctctgga gggattgctc aaagccctga 350

gccaggctag cacagatcct aaggaatcaa catctcccga gaaacgtgac 400

atgcatgact tctttgtggg acttatgggc aagaggagcg tccagccaga 450

gggaaagaca ggacctttct taccttcagt gagggttcct cggccccttc 500

atcccaatca gcttggatcc acaggaaagt cttccctggg aacagaggag 550

cagagacctt tataagactc tcctacggat gtgaatcaag agaacgtccc 600

cagctttggc atcctcaagt atcccccgag agcagaatag gtactccact 650

tccggactcc tggactgcat taggaagacc tctttccctg tcccaatccc 700

caggtgcgca cgctcctgtt acccttctc ttccctgttc ttgtaacatt 750

cttgtgcttt gactccttct ccatcttttc tacctgaccc tggtgtggaa 800

actgcatagt gaatatcccc aaccccaatg ggcattgact gtagaatacc 850

ctagagttcc tgtagtgtcc tacattaaaa atataatgtc tctctctatt 900

cctcaacaat aaaggatttt tgcatatgaa aaaaaaaaaa aaaaaaaaaa 950

aaaaaaaaaa aaaaaaaaaa aa 972

<210> 359
<211> 135
<212> PRT
<213> Homo sapiens

<400> 359

Met	Arg	Ile	Met	Leu	Leu	Phe	Thr	Ala	Ile	Leu	Ala	Phe	Ser	Leu	
1				5				10						15	
Ala	Gln	Ser	Phe	Gly	Ala	Val	Cys	Lys	Glu	Pro	Gln	Glu	Glu	Val	
				20				25						30	
Val	Pro	Gly	Gly	Gly	Arg	Ser	Lys	Arg	Asp	Pro	Asp	Leu	Tyr	Gln	
				35				40						45	
Leu	Leu	Gln	Arg	Leu	Phe	Lys	Ser	His	Ser	Ser	Leu	Glu	Gly	Leu	
				50				55						60	
Leu	Lys	Ala	Leu	Ser	Gln	Ala	Ser	Thr	Asp	Pro	Lys	Glu	Ser	Thr	
				65				70						75	
Ser	Pro	Glu	Lys	Arg	Asp	Met	His	Asp	Phe	Phe	Val	Gly	Leu	Met	
				80				85						90	
Gly	Lys	Arg	Ser	Val	Gln	Pro	Glu	Gly	Lys	Thr	Gly	Pro	Phe	Leu	
				95				100						105	
Pro	Ser	Val	Arg	Val	Pro	Arg	Pro	Leu	His	Pro	Asn	Gln	Leu	Gly	
				110				115						120	

Ser Thr Gly Lys Ser Ser Leu Gly Thr Glu Glu Gln Arg Pro Leu
125 130 135

<210> 360
<211> 1738
<212> DNA
<213> Homo sapiens

<400> 360
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gcctgctgtg cccgcgctgt cgccgctgct accgcgtctg ctggacgcgg 100

gagacgccag cgagctggtg attggagccc tgcggagagc tcaagcgccc 150

agctctgccc caggagccca ggctgccccg tgagtcccat agttgctgca 200

ggagtggagc catgagctgc gtcctgggtg gtgtcatccc cttggggctg 250

ctgttcctgg tctgcggatc ccaaggctac ctcctgccca acgtcactct 300

cttagaggag ctgctcagca aataccagca caacgagtct cactcccggg 350

tccgcagagc catccccagg gaggacaagg aggagatcct catgctgcac 400

aacaagcttc ggggccaggt gcagcctcag gcctccaaca tggagtacat 450

ggtgagcgcc ggctccggcc gcagaggctg gcaccggggg tggggcctgg 500

gccaccagcc tgctctgttc cccagccagc tctgttcccc agccagtgcg 550

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ctggagtgca atggcacaat cgtcatgccc tgaaacctta gactcccggg 700

gttaagcgat cctgcttcag cctcccaagt agctggaact acaggcatgc 750

accatggtgc ccagctagat tttaaatatt ttgtggagat gggggtcttg 800

ctacgttgcc caggctggtc ttgaactcct aggctcaagc aatcctcctg 850

cctcagcctc tcaaagtgct aggattatag gcatgagtca ccctgtctgg 900

ctctggctct gttcttaaca ttctgccaaa acaacacacg tgggttccct 950

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agtccttcct cgcgtggttg ccatgactgt gagataagtc gaggctgtga 1200

agggcccggc acagactgac ctgcctcccc aacccctagg ctttgctaac 1250

cgggaaagga gctaacggtg acagaagaca gccaaggtca accctcccgg 1300

gtgattgtga tgggtgttcc aggtgtggtt gggcgatgct gctacttgac 1350

cccaagctcc agtgtggaaa cttccttcct ggctggtttt ccagaactac 1400

agaggaatgg accacagtct tccagggtcc ctcctcgtcc accaaccggg 1450

agcctccacc ttggccatcc gtcagctatg aatggctttt taaacaaacc 1500

cacgtcccag cctgggtaac atggtaaagc cccgtctcta caaaaaaatc 1550

caagttagcc gggcatggtg gtgcgcacct gtagtcccag ctgcagtggg 1600

actgaggtgg aggtggaggt gggggggtggg agctgaggaa ggaggatcgc 1650

ttgagcctgg gaagtcgagg ctgcagtgag ctgagattgc accactgcac 1700

tccagcctgg gtgacagagc aagaccctgt ctcaaaaa 1738

<210> 361
<211> 159
<212> PRT
<213> Homo sapiens

<400> 361

Met	Ser	Cys	Val	Leu	Gly	Gly	Val	Ile	Pro	Leu	Gly	Leu	Leu	Phe	
1				5					10					15	
Leu	Val	Cys	Gly	Ser	Gln	Gly	Tyr	Leu	Leu	Pro	Asn	Val	Thr	Leu	
				20					25					30	
Leu	Glu	Glu	Leu	Leu	Ser	Lys	Tyr	Gln	His	Asn	Glu	Ser	His	Ser	
				35					40					45	
Arg	Val	Arg	Arg	Ala	Ile	Pro	Arg	Glu	Asp	Lys	Glu	Glu	Ile	Leu	
				50					55					60	
Met	Leu	His	Asn	Lys	Leu	Arg	Gly	Gln	Val	Gln	Pro	Gln	Ala	Ser	
				65					70					75	
Asn	Met	Glu	Tyr	Met	Val	Ser	Ala	Gly	Ser	Gly	Arg	Arg	Gly	Trp	
				80					85					90	
His	Arg	Gly	Trp	Gly	Leu	Gly	His	Gln	Pro	Ala	Leu	Phe	Pro	Ser	
				95					100					105	
Gln	Leu	Cys	Ser	Pro	Ala	Ser	Ala	Cys	Asp	Gly	Trp	Leu	Arg	Val	
				110					115					120	
Ser	Ser	Gly	Arg	Gly	Gly	Ser	Arg	Leu	Cys	Ser	Val	Leu	Phe	Val	
				125					130					135	
Cys	Phe	Glu	Thr	Gly	Ser	His	Ser	Ala	Thr	Asp	Ala	Gly	Val	Gln	
				140					145					150	
Trp	His	Asn	Arg	His	Ala	Leu	Lys	Pro							
				155											

<210> 362
<211> 422
<212> DNA
<213> Homo sapiens

<400> 362
aaggagaggc caccgggact tcagtgtctc ctccatccca ggagcgcagt 50

ggccactatg gggtctgggc tgccccttgt cctcctcttg accctccttg 100

gcagctcaca tggaacaggg ccgggtatga ctttgcaact gaagctgaag 150

gagtcttttc tgacaaattc ctcctatgag tccagcttcc tggaattgct 200

tgaaaagctc tgcctcctcc tccatctccc ttcagggacc agcgtcaccc 250

tccaccatgc aagatctcaa caccatgttg tctgcaacac atgacagcca 300

ttgaagcctg tgtccttctt ggcccgggct tttgggccgg ggatgcagga 350

ggcaggcccc gaccctgtct ttcagcaggc ccccaccctc ctgagtggca 400

ataaataaaa ttcggtatgc tg 422

<210> 363
<211> 78
<212> PRT
<213> Homo sapiens

<400> 363

Met	Gly	Ser	Gly	Leu	Pro	Leu	Val	Leu	Leu	Leu	Thr	Leu	Leu	Gly	
1				5				10						15	
Ser	Ser	His	Gly	Thr	Gly	Pro	Gly	Met	Thr	Leu	Gln	Leu	Lys	Leu	
			20					25						30	
Lys	Glu	Ser	Phe	Leu	Thr	Asn	Ser	Ser	Tyr	Glu	Ser	Ser	Phe	Leu	
			35					40						45	
Glu	Leu	Leu	Glu	Lys	Leu	Cys	Leu	Leu	Leu	His	Leu	Pro	Ser	Gly	
			50					55						60	
Thr	Ser	Val	Thr	Leu	His	His	Ala	Arg	Ser	Gln	His	His	Val	Val	
			65					70						75	

Cys Asn Thr

<210> 364
<211> 826
<212> DNA
<213> Homo sapiens

<400> 364
aattgtatct gtgtaatgtt aaaacaaacg aaataaaata gaaggaaaaa 50

ctttctgagt ttcaaaaaca acagactagt actctaaaga actctttaaa 100

acaattaact gttaggattg cagttatgat tggatattat ttaattctgt 150

ttctgatgtg gggttcctcc actgtgttct gtgtgctatt aatatttacc 200

attgcagaag cttcattcag tgttgaaaat gaatgcttag tggatctgtg 250

cctcttacgc atatgttaca aattatctgg agttcctaat caatgcagag 300

ttcccctccc ctccgattgt tctaaataat tgaaagatgt ctgctgtgga 350

aaaaggcatg tatttaaatc tgtatgattc tcaaccatct ttagttggga 400

aaggtccttg aaagccaatg gaaatacttt ttttttttct tggcactaat 450

caagtgagtg ttacctttc acttagtagg atgtgttgtt acgctagtaa 500

aatagaaacc tgtgtttatt ctcaggtatt ttagaaacaa cagccatcat 550

tttattttat gtgtgtgttc ttggctgtat tcataaatta tatattttgg 600

gctatcaaat attacttcat tcaatataaa taacaatagt agaagttgtt 650

tacttagata tgctttctag ttgcattttc tcagcctatg taagactact 700

ttgttgtaat agcctttgaa atttacagta ctgtctctct actatcttca 750

gattacttga ttcaaataaa ccaattatgt ttgtaattga tattaataaa 800

accagaataa aagttcatat ctaccc 826

<210> 365
<211> 67
<212> PRT
<213> Homo sapiens

<400> 365

Met	Ile	Gly	Tyr	Tyr	Leu	Ile	Leu	Phe	Leu	Met	Trp	Gly	Ser	Ser	
1				5				10						15	
Thr	Val	Phe	Cys	Val	Leu	Leu	Ile	Phe	Thr	Ile	Ala	Glu	Ala	Ser	
				20				25						30	
Phe	Ser	Val	Glu	Asn	Glu	Cys	Leu	Val	Asp	Leu	Cys	Leu	Leu	Arg	
				35				40						45	
Ile	Cys	Tyr	Lys	Leu	Ser	Gly	Val	Pro	Asn	Gln	Cys	Arg	Val	Pro	
				50				55						60	
Leu	Pro	Ser	Asp	Cys	Ser	Lys									
				65											

<210> 366
<211> 2475
<212> DNA
<213> Homo sapiens

<400> 366
gaggatttgc cacagcagcg gatagagcag gagagcacca ccggagccct 50

tgagacatcc ttgagaagag ccacagcata agagactgcc ctgcttggtg 100

ttttgcagga tgatggtggc ccttcgagga gcttctgcat tgctggttct 150

gttccttgca gcttttctgc ccccgccgca gtgtacccag gacccagcca 200

tggtgcatta catctaccag cgctttcgag tcttggagca agggctggaa 250

aaatgtaccc aagcaacgag ggcatacatt caagaattcc aagagttctc 300

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acaagagtgc agtgggtaac ttggcactga gagttgaacg tgcccaacgg 400

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agaggacaag acactggcag aaatgttgct ccaagaagct gaagaagaga 500

aaaagatccg gactctgctg aatgcaagct gtgacaacat gctgatgggc 550

ataaagtctt tgaaaatagt gaagaagatg atggacacac atggctcttg 600

gatgaaagat gctgtctata actctccaaa ggtgtactta ttaattggat 650

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atgcctggaa tgaaggaaac cagatcattt acaaactcca gacaaagaga 1300

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cagttttcat gtctgcacaa gacctttcaa taggcctttc aaatgataat 2350

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gacactgagc aaaaaaaaaa aaaaa 2475

<210> 367
<211> 402
<212> PRT
<213> Homo sapiens

<400> 367

Met	Met	Val	Ala	Leu	Arg	Gly	Ala	Ser	Ala	Leu	Leu	Val	Leu	Phe	
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Leu	Ala	Ala	Phe	Leu	Pro	Pro	Pro	Gln	Cys	Thr	Gln	Asp	Pro	Ala	
			20					25						30	
Met	Val	His	Tyr	Ile	Tyr	Gln	Arg	Phe	Arg	Val	Leu	Glu	Gln	Gly	
			35					40						45	
Leu	Glu	Lys	Cys	Thr	Gln	Ala	Thr	Arg	Ala	Tyr	Ile	Gln	Glu	Phe	
			50					55						60	
Gln	Glu	Phe	Ser	Lys	Asn	Ile	Ser	Val	Met	Leu	Gly	Arg	Cys	Gln	
			65					70						75	
Thr	Tyr	Thr	Ser	Glu	Tyr	Lys	Ser	Ala	Val	Gly	Asn	Leu	Ala	Leu	
			80					85						90	
Arg	Val	Glu	Arg	Ala	Gln	Arg	Glu	Ile	Asp	Tyr	Ile	Gln	Tyr	Leu	
			95					100						105	
Arg	Glu	Ala	Asp	Glu	Cys	Ile	Val	Ser	Glu	Asp	Lys	Thr	Leu	Ala	
			110					115						120	
Glu	Met	Leu	Leu	Gln	Glu	Ala	Glu	Glu	Glu	Lys	Lys	Ile	Arg	Thr	
			125					130						135	
Leu	Leu	Asn	Ala	Ser	Cys	Asp	Asn	Met	Leu	Met	Gly	Ile	Lys	Ser	
			140					145						150	
Leu	Lys	Ile	Val	Lys	Lys	Met	Met	Asp	Thr	His	Gly	Ser	Trp	Met	
			155					160						165	
Lys	Asp	Ala	Val	Tyr	Asn	Ser	Pro	Lys	Val	Tyr	Leu	Leu	Ile	Gly	
			170					175						180	
Ser	Arg	Asn	Asn	Thr	Val	Trp	Glu	Phe	Ala	Asn	Ile	Arg	Ala	Phe	
			185					190						195	
Met	Glu	Asp	Asn	Thr	Lys	Pro	Ala	Pro	Arg	Lys	Gln	Ile	Leu	Thr	
			200					205						210	

Leu Ser Trp Gln Gly Thr Gly Gln Val Ile Tyr Lys Gly Phe Leu
215 220 225

Phe Phe His Asn Gln Ala Thr Ser Asn Glu Ile Ile Lys Tyr Asn
230 235 240

Leu Gln Lys Arg Thr Val Glu Asp Arg Met Leu Leu Pro Gly Gly
245 250 255

Val Gly Arg Ala Leu Val Tyr Gln His Ser Pro Ser Thr Tyr Ile
260 265 270

Asp Leu Ala Val Asp Glu His Gly Leu Trp Ala Ile His Ser Gly
275 280 285

Pro Gly Thr His Ser His Leu Val Leu Thr Lys Ile Glu Pro Gly
290 295 300

Thr Leu Gly Val Glu His Ser Trp Asp Thr Pro Cys Arg Ser Gln
305 310 315

Asp Ala Glu Ala Ser Phe Leu Leu Cys Gly Val Leu Tyr Val Val
320 325 330

Tyr Ser Thr Gly Gly Gln Gly Pro His Arg Ile Thr Cys Ile Tyr
335 340 345

Asp Pro Leu Gly Thr Ile Ser Glu Glu Asp Leu Pro Asn Leu Phe
350 355 360

Phe Pro Lys Arg Pro Arg Ser His Ser Met Ile His Tyr Asn Pro
365 370 375

Arg Asp Lys Gln Leu Tyr Ala Trp Asn Glu Gly Asn Gln Ile Ile
380 385 390

Tyr Lys Leu Gln Thr Lys Arg Lys Leu Pro Leu Lys
395 400

<210> 368
<211> 2281
<212> DNA
<213> Homo sapiens

<400> 368
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ggaggagagg agcggccggc ccgcctgcca aaaagcaaat ggatttccac 200

ctgacaaatc ttcgggatcc aagaagcaga aacaatatca gcggattcgg 250

aaggagaagc ctcaacaaca caacttcacc caccgcctcc tggctgcagc 300

tctgaagagc cacagcggga acatatcttg catggacttt agcagcaatg 350

gcaaatacct ggctacctgt gcagatgatc gcaccatccg catctggagc 400

accaaggact tcctgcagcg agagcaccgc agcatgagag ccaacgtgga 450

gctggaccac gccaccctgg tgcgcttcag ccctgactgc agagccttca 500

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atgtgaaggt ttgggaagtc tgctttggaa agaaggggga gttccaggag 850

gtggtgcgag ccttcgaact aaagggccac tccgcggctg tgcactcgtt 900

tgctttctcc aacgactcac ggaggatggc ttctgtctcc aaggatggta 950

catggaaact gtgggacaca gatgtggaat acaagaagaa gcaggacccc 1000

tacttgctga agacaggccg ctttgaagag gcggcgggtg ccgcgccgtg 1050

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agaacaacct agagaacacc tgagtactaa gcagcagttt tgcaaggatg 1800

ggagactggg atagcttccc atcacagaac tgtgttccat caaaaagaca 1850

ctaagggatt tccttctggg cctcagttct atttgtaaga tggagaataa 1900

tcctctctgt gaactccttg caaagatgat atgaggctaa gagaatatca 1950

agtccccagg tctggaagaa aagtagaaaa gagtagtact attgtccaat 2000

gtcatgaaag tggtaaaagt gggaaccagt gtgctttgaa accaaattag 2050

aaacacattc cttgggaagg caaagtttc tgggacttga tcatacattt 2100

tatatggttg ggacttctct cttcgggaga tgatatcttg tttaaggaga 2150

cctcttttca gttcatcaag ttcatcagat atttgagtgc ccactctgtg 2200

cccaaataaa tatgagctgg ggattaaaaa aaaaaaaaaa aaaaaaaaaa 2250

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 2281

<210> 369
<211> 447
<212> PRT
<213> Homo sapiens

<400> 369

Met	Glu	Leu	Ser	Gln	Met	Ser	Glu	Leu	Met	Gly	Leu	Ser	Val	Leu	
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Leu	Gly	Leu	Leu	Ala	Leu	Met	Ala	Thr	Ala	Ala	Val	Ala	Arg	Gly	
				20					25						30
Trp	Leu	Arg	Ala	Gly	Glu	Glu	Arg	Ser	Gly	Arg	Pro	Ala	Cys	Gln	
				35					40						45
Lys	Ala	Asn	Gly	Phe	Pro	Pro	Asp	Lys	Ser	Ser	Gly	Ser	Lys	Lys	
				50					55						60
Gln	Lys	Gln	Tyr	Gln	Arg	Ile	Arg	Lys	Glu	Lys	Pro	Gln	Gln	His	
				65					70						75
Asn	Phe	Thr	His	Arg	Leu	Leu	Ala	Ala	Ala	Leu	Lys	Ser	His	Ser	
				80					85						90
Gly	Asn	Ile	Ser	Cys	Met	Asp	Phe	Ser	Ser	Asn	Gly	Lys	Tyr	Leu	
				95					100						105
Ala	Thr	Cys	Ala	Asp	Asp	Arg	Thr	Ile	Arg	Ile	Trp	Ser	Thr	Lys	
				110					115						120
Asp	Phe	Leu	Gln	Arg	Glu	His	Arg	Ser	Met	Arg	Ala	Asn	Val	Glu	
				125					130						135
Leu	Asp	His	Ala	Thr	Leu	Val	Arg	Phe	Ser	Pro	Asp	Cys	Arg	Ala	
				140					145						150
Phe	Ile	Val	Trp	Leu	Ala	Asn	Gly	Asp	Thr	Leu	Arg	Val	Phe	Lys	
				155					160						165
Met	Thr	Lys	Arg	Glu	Asp	Gly	Gly	Tyr	Thr	Phe	Thr	Ala	Thr	Pro	
				170					175						180
Glu	Asp	Phe	Pro	Lys	Lys	His	Lys	Ala	Pro	Val	Ile	Asp	Ile	Gly	
				185					190						195
Ile	Ala	Asn	Thr	Gly	Lys	Phe	Ile	Met	Thr	Ala	Ser	Ser	Asp	Thr	
				200					205						210
Thr	Val	Leu	Ile	Trp	Ser	Leu	Lys	Gly	Gln	Val	Leu	Ser	Thr	Ile	
				215					220						225
Asn	Thr	Asn	Gln	Met	Asn	Asn	Thr	His	Ala	Ala	Val	Ser	Pro	Cys	
				230					235						240

Gly Arg Phe Val Ala Ser Cys Gly Phe Thr Pro Asp Val Lys Val
245 250 255

Trp Glu Val Cys Phe Gly Lys Lys Gly Glu Phe Gln Glu Val Val
260 265 270

Arg Ala Phe Glu Leu Lys Gly His Ser Ala Ala Val His Ser Phe
275 280 285

Ala Phe Ser Asn Asp Ser Arg Arg Met Ala Ser Val Ser Lys Asp
290 295 300

Gly Thr Trp Lys Leu Trp Asp Thr Asp Val Glu Tyr Lys Lys Lys
305 310 315

Gln Asp Pro Tyr Leu Leu Lys Thr Gly Arg Phe Glu Glu Ala Ala
320 325 330

Gly Ala Ala Pro Cys Arg Leu Ala Leu Ser Pro Asn Ala Gln Val
335 340 345

Leu Ala Leu Ala Ser Gly Ser Ser Ile His Leu Tyr Asn Thr Arg
350 355 360

Arg Gly Glu Lys Glu Glu Cys Phe Glu Arg Val His Gly Glu Cys
365 370 375

Ile Ala Asn Leu Ser Phe Asp Ile Thr Gly Arg Phe Leu Ala Ser
380 385 390

Cys Gly Asp Arg Ala Val Arg Leu Phe His Asn Thr Pro Gly His
395 400 405

Arg Ala Met Val Glu Glu Met Gln Gly His Leu Lys Arg Ala Ser
410 415 420

Asn Glu Ser Thr Arg Gln Arg Leu Gln Gln Gln Leu Thr Gln Ala
425 430 435

Gln Glu Thr Leu Lys Ser Leu Gly Ala Leu Lys Lys
440 445

<210> 370
<211> 1415
<212> DNA
<213> Homo sapiens

<400> 370
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ccacgcgagt ctcaatcatg ctcctcctag taactgtgtc tgactgtgct 150

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aggaaacgca agcaccacac ctgtccttgc ttgcccaacc tgctgtgctc 350

caggttcccg gacggcaggt accgctgctc catggacttg aagaacatca 400

atttttaggc gcttgcctgg tctcaggata cccaccatcc ttttcctgag 450

cacagcctgg atttttattt ctgccatgaa acccagctcc catgactctc 500

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tcagaccagg gaggcaacta cacaccaaca tgctggcttt agaataaaag 1400

caccaactga aaaaa 1415

<210> 371
<211> 105
<212> PRT
<213> Homo sapiens

<400> 371

Met	Arg	Gly	Ala	Thr	Arg	Val	Ser	Ile	Met	Leu	Leu	Leu	Val	Thr	
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Val	Ser	Asp	Cys	Ala	Val	Ile	Thr	Gly	Ala	Cys	Glu	Arg	Asp	Val	
				20					25					30	
Gln	Cys	Gly	Ala	Gly	Thr	Cys	Cys	Ala	Ile	Ser	Leu	Trp	Leu	Arg	
				35					40					45	
Gly	Leu	Arg	Met	Cys	Thr	Pro	Leu	Gly	Arg	Glu	Gly	Glu	Glu	Cys	
				50					55					60	
His	Pro	Gly	Ser	His	Lys	Val	Pro	Phe	Phe	Arg	Lys	Arg	Lys	His	
				65					70					75	

His Thr Cys Pro Cys Leu Pro Asn Leu Leu Cys Ser Arg Phe Pro
80 85 90

Asp Gly Arg Tyr Arg Cys Ser Met Asp Leu Lys Asn Ile Asn Phe
95 100 105

<210> 372
<211> 1281
<212> DNA
<213> Homo sapiens

<400> 372
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gaaatgtctt tcctccagga cccaagtttc ttcaccatgg ggatgtggtc 100

cattggtgca ggagccctgg gggctgctgc cttggcattg ctgcttgcca 150

acacagacgt gtttctgtcc aagccccaga aagcggccct ggagtacctg 200

gaggatatag acctgaaaac actggagaag gaaccaagga ctttcaaagc 250

aaaggagcta tgggaaaaaa atggagctgt gattatggcc gtgcggaggc 300

caggctgttt cctctgtcga gaggaagctg cggatctgtc ctccctgaaa 350

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catcaggact gaagtgaagg atttccagcc ttatttcaaa ggagaaatct 450

tcctggatga aaagaaaaag ttctatggtc cacaaaggcg gaagatgatg 500

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gaacggaggc ttctctggaa acctggaagg agaaggcttc atccttgggg 600

gagttttcgt ggtgggatca ggaaagcagg gcattcttct tgagcaccga 650

gaaaaagaat ttggagacaa agtaaaccta ctttctgttc tggaagctgc 700

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tgtattgttt ccactcgtgt ccctaaggag tgagaaaccc atttatactc 850

tactctcagt atggattatt aatgtatttt aatattctgt ttaggcccac 900

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caggctgggt gcagtggctc acacctgtaa tcccagcact ttgggaggcc 1050

aaggtgagca agtcacttga ggtcgggagt tcgagaccag cctgagcaac 1100

atggcgaaac cccgtctcta ctaaaaatac aaaaatcacc cgggtgtggt 1150

ggcaggcacc tgtagtccca gctacccggg aggctgaggc aggagaatca 1200

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ttccagcctg ggtgactgag actctaacta a 1281

<210> 373
<211> 229
<212> PRT
<213> Homo sapiens

<400> 373
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Ser Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu
20 25 30

Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala
35 40 45

Leu Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu
50 55 60

Pro Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala
65 70 75

Val Ile Met Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu
80 85 90

Glu Ala Ala Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu
95 100 105

Gly Val Pro Leu Tyr Ala Val Val Lys Glu His Ile Arg Thr Glu
110 115 120

Val Lys Asp Phe Gln Pro Tyr Phe Lys Gly Glu Ile Phe Leu Asp
125 130 135

Glu Lys Lys Lys Phe Tyr Gly Pro Gln Arg Arg Lys Met Met Phe
140 145 150

Met Gly Phe Ile Arg Leu Gly Val Trp Tyr Asn Phe Phe Arg Ala
155 160 165

Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly Glu Gly Phe Ile
170 175 180

Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln Gly Ile Leu
185 190 195

Leu Glu His Arg Glu Lys Glu Phe Gly Asp Lys Val Asn Leu Leu
200 205 210

Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln Thr Leu Ala
215 220 225

Ser Glu Lys Lys

<210> 374
<211> 744
<212> DNA
<213> Homo sapiens

<400> 374
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caaagacgcc cgggccaggt gccccgtcgc aggtgcccct ggccggagat 100

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gccacccagc ccatggcgaa ccccgggctg gggctgcttc tggcgctggg 200

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agactctgcc cctgaggtca agagaggatg gggctattca cttttatata 700

tttatataaa attagtagtg agatgtaaaa aaaaaaaaaa aaaa 744

<210> 375
<211> 123
<212> PRT
<213> Homo sapiens

<400> 375

Met	Ala	Asn	Pro	Gly	Leu	Gly	Leu	Leu	Leu	Ala	Leu	Gly	Leu	Pro	
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Phe	Leu	Leu	Ala	Arg	Trp	Gly	Arg	Ala	Trp	Gly	Gln	Ile	Gln	Thr	
				20				25						30	
Thr	Ser	Ala	Asn	Glu	Asn	Ser	Thr	Val	Leu	Pro	Ser	Ser	Thr	Ser	
				35				40						45	
Ser	Ser	Ser	Asp	Gly	Asn	Leu	Arg	Pro	Glu	Ala	Ile	Thr	Ala	Ile	
				50				55						60	
Ile	Val	Val	Phe	Ser	Leu	Leu	Ala	Ala	Leu	Leu	Leu	Ala	Val	Gly	
				65				70						75	
Leu	Ala	Leu	Leu	Val	Arg	Lys	Leu	Arg	Glu	Lys	Arg	Gln	Thr	Glu	
				80				85						90	
Gly	Thr	Tyr	Arg	Pro	Ser	Ser	Glu	Glu	Gln	Phe	Ser	His	Ala	Ala	
				95				100						105	
Glu	Ala	Arg	Ala	Pro	Gln	Asp	Ser	Lys	Glu	Thr	Val	Gln	Gly	Cys	
				110				115						120	

Leu Pro Ile

<210> 376
<211> 713
<212> DNA
<213> Homo sapiens

<400> 376
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aacatttggg ttttgggatt ttaattttca aacacagcag aatgacattt 100

tttctgtcac tattattatt gttggtatgt gaagctattt ggagatccaa 150

ttcaggaagc aacacattgg agaatggcta ctttctatca agaaataaag 200

agaaccacag tcaacccaca caatcatctt tagaagacag tgtgactcct 250

accaaagctg tcaaaaccac aggcaagggc atagttaaag gacggaatct 300

tgactcaaga gggttaattc ttggtgctga agcctggggc aggggtgtaa 350

agaaaaacac ttagattcaa tgattgtaaa tttaaggcaa atacacatat 400

tagtattacc ttagtgtaat gtatccctgt catatataca ataaggtgaa 450

attataagta ccctatgcag ttggctggac agttctaaat tggactttat 500

taatttttaa aatcagtaac tgatttatca ctggctatgt gcttagatct 550

acaggagatc atataatttg atacaaataa aagaaaagtg ttctctcccc 600

ttacagaatt gacattttaa atgcgataca gttagaatag gaaatatgac 650

attagaaagg aagaatgaca gggagaaagg aaagaaggga aaatgttgcc 700

aaggaaaaaa aaa 713

<210> 377
<211> 90
<212> PRT
<213> Homo sapiens

<400> 377
Met Thr Phe Phe Leu Ser Leu Leu Leu Leu Leu Val Cys Glu Ala
1 5 10 15

Ile Trp Arg Ser Asn Ser Gly Ser Asn Thr Leu Glu Asn Gly Tyr
20 25 30

Phe Leu Ser Arg Asn Lys Glu Asn His Ser Gln Pro Thr Gln Ser
35 40 45

Ser Leu Glu Asp Ser Val Thr Pro Thr Lys Ala Val Lys Thr Thr
50 55 60

Gly Lys Gly Ile Val Lys Gly Arg Asn Leu Asp Ser Arg Gly Leu
65 70 75

Ile Leu Gly Ala Glu Ala Trp Gly Arg Gly Val Lys Lys Asn Thr
80 85 90

<210> 378
<211> 3265
<212> DNA
<213> Homo sapiens

<400> 378
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cctcttagtt ctgtgcctgc tgcaccagtc aaatacttcc ttcattaagc 100

tgaataataa tggctttgaa gatattgtca ttgttataga tcctagtgtg 150

ccagaagatg aaaaaataat tgaacaaata gaggatatgg tgactacagc 200

ttctacgtac ctgtttgaag ccacagaaaa aagatttttt ttcaaaaatg 250

tatctatatt aattcctgag aattggaagg aaaatcctca gtacaaaagg 300

ccaaaacatg aaaaccataa acatgctgat gttatagttg caccacctac 350

actcccaggt agagatgaac catacaccaa gcagttcaca gaatgtggag 400

agaaaggcga atacattcac ttcacccctg accttctact tggaaaaaaa 450

caaaatgaat atggaccacc aggcaaactg tttgtccatg agtgggctca 500

cctccggtgg ggagtgtttg atgagtacaa tgaagatcag cctttctacc 550

gtgctaagtc aaaaaaaatc gaagcaacaa ggtgttccgc aggtatctct 600

ggtagaaata gagtttataa gtgtcaagga ggcagctgtc ttagtagagc 650

atgcagaatt gattctacaa caaaactgta tggaaaagat tgtcaattct 700

ttcctgataa agtacaaaca gaaaaagcat ccataatgtt tatgcaaagt 750

attgattctg ttgttgaatt ttgtaacgaa aaaacccata atcaagaagc 800

tccaagccta caaaacataa agtgcaattt tagaagtaca tgggaggtga 850

ttagcaattc tgaggatttt aaaaacacca tacccatggt gacaccacct 900

cctccacctg tcttctcatt gctgaagatc agtcaaagaa ttgtgtgctt 950

agttcttgat aagtctggaa gcatgggggg taaggaccgc ctaaatcgaa 1000

tgaatcaagc agcaaaacat ttcctgctgc agactgttga aaatggatcc 1050

tgggtgggga tggttcactt tgatagtact gccactattg taaataagct 1100

aatccaaata aaaagcagtg atgaaagaaa cacactcatg gcaggattac 1150

ctacatatcc tctgggagga acttccatct gctctggaat taaatatgca 1200

tttcaggtga ttggagagct acattcccaa ctcgatggat ccgaagtact 1250

gctgctgact gatggggagg ataacactgc aagttcttgt attgatgaag 1300

tgaaacaaag tggggccatt gttcatttta ttgctttggg aagagctgct 1350

gatgaagcag taatagagat gagcaagata acaggaggaa gtcattttta 1400

tgtttcagat gaagctcaga acaatggcct cattgatgct tttggggctc 1450

ttacatcagg aaatactgat ctctcccaga agtcccttca gctcgaaagt 1500

aagggattaa cactgaatag taatgcctgg atgaacgaca ctgtcataat 1550

tgatagtaca gtgggaaagg acacgttctt tctcatcaca tggaacagtc 1600

tgcctcccag tatttctctc tgggatccca gtggaacaat aatggaaaat 1650

ttcacagtgg atgcaacttc caaaatggcc tatctcagta ttccaggaac 1700

tgcaaaggtg ggcacttggg catacaatct tcaagccaaa gcgaacccag 1750

aaacattaac tattacagta acttctcgag cagcaaattc ttctgtgcct 1800

ccaatcacag tgaatgctaa aatgaataag gacgtaaaca gtttccccag 1850

cccaatgatt gtttacgcag aaattctaca aggatatgta cctgttcttg 1900

gagccaatgt gactgctttc attgaatcac agaatggaca tacagaagtt 1950

ttggaacttt tggataatgg tgcaggcgct gattctttca agaatgatgg 2000

agtctactcc aggtatttta cagcatatac agaaaatggc agatatagct 2050

taaaagttcg ggctcatgga ggagcaaaca ctgccaggct aaaattacgg 2100

cctccactga atagagccgc gtacatacca ggctgggtag tgaacgggga 2150

aattgaagca aacccgccaa gacctgaaat tgatgaggat actcagacca 2200

ccttggagga tttcagccga acagcatccg gaggtgcatt tgtggtatca 2250

caagtcccaa gccttccctt gcctgaccaa tacccaccaa gtcaaatcac 2300

agaccttgat gccacagttc atgaggataa gattattctt acatggacag 2350

caccaggaga taattttgat gttggaaaag ttcaacgtta tatcataaga 2400

ataagtgcaa gtattcttga tctaagagac agttttgatg atgctcttca 2450

agtaaatact actgatctgt caccaaagga ggccaactcc aaggaaagct 2500

ttgcatttaa accagaaaat atctcagaag aaaatgcaac ccacatattt 2550

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cattgcacaa gtaactttgt ttatccctca agcaaatcct gatgacattg 2650

atcctacacc tactcctact cctactccta ctcctgataa aagtcataat 2700

tctggagtta atatttctac gctggtattg tctgtgattg ggtctgttgt 2750

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aacactcatg gatatgtaaa aactgtcaag attaaaattt aatagtttca 3000

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tcatactgat acctggttgt atattatttg atgcaacagt tttctgaaat 3100

gatatttcaa attgcatcaa gaaattaaaa tcatctatct gagtagtcaa 3150

aatacaagta aaggagagca aataaacaac atttggaaaa aaaaaaaaaa 3200

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3250

aaaaaaaaaa aaaaa 3265

<210> 379
<211> 919
<212> PRT
<213> Homo sapiens

<400> 379

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Met Gly Leu Phe Arg Gly Phe Val Phe Leu Leu Val Leu Cys Leu
  1               5                  10                  15

Leu His Gln Ser Asn Thr Ser Phe Ile Lys Leu Asn Asn Asn Gly
             20                  25                  30

Phe Glu Asp Ile Val Ile Val Ile Asp Pro Ser Val Pro Glu Asp
             35                  40                  45

Glu Lys Ile Ile Glu Gln Ile Glu Asp Met Val Thr Thr Ala Ser
             50                  55                  60

Thr Tyr Leu Phe Glu Ala Thr Glu Lys Arg Phe Phe Phe Lys Asn
             65                  70                  75

Val Ser Ile Leu Ile Pro Glu Asn Trp Lys Glu Asn Pro Gln Tyr
             80                  85                  90

Lys Arg Pro Lys His Glu Asn His Lys His Ala Asp Val Ile Val
             95                 100                 105

Ala Pro Pro Thr Leu Pro Gly Arg Asp Glu Pro Tyr Thr Lys Gln
            110                 115                 120

Phe Thr Glu Cys Gly Glu Lys Gly Glu Tyr Ile His Phe Thr Pro
            125                 130                 135

Asp Leu Leu Leu Gly Lys Lys Gln Asn Glu Tyr Gly Pro Pro Gly
            140                 145                 150

Lys Leu Phe Val His Glu Trp Ala His Leu Arg Trp Gly Val Phe
            155                 160                 165

Asp Glu Tyr Asn Glu Asp Gln Pro Phe Tyr Arg Ala Lys Ser Lys
            170                 175                 180

Lys Ile Glu Ala Thr Arg Cys Ser Ala Gly Ile Ser Gly Arg Asn
            185                 190                 195

Arg Val Tyr Lys Cys Gln Gly Gly Ser Cys Leu Ser Arg Ala Cys
            200                 205                 210

Arg Ile Asp Ser Thr Thr Lys Leu Tyr Gly Lys Asp Cys Gln Phe
            215                 220                 225

Phe Pro Asp Lys Val Gln Thr Glu Lys Ala Ser Ile Met Phe Met
            230                 235                 240

Gln Ser Ile Asp Ser Val Val Glu Phe Cys Asn Glu Lys Thr His
            245                 250                 255

Asn Gln Glu Ala Pro Ser Leu Gln Asn Ile Lys Cys Asn Phe Arg
            260                 265                 270

Ser Thr Trp Glu Val Ile Ser Asn Ser Glu Asp Phe Lys Asn Thr
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275 280 285

Ile Pro Met Val Thr Pro Pro Pro Pro Pro Val Phe Ser Leu Leu
290 295 300

Lys Ile Ser Gln Arg Ile Val Cys Leu Val Leu Asp Lys Ser Gly
305 310 315

Ser Met Gly Gly Lys Asp Arg Leu Asn Arg Met Asn Gln Ala Ala
320 325 330

Lys His Phe Leu Leu Gln Thr Val Glu Asn Gly Ser Trp Val Gly
335 340 345

Met Val His Phe Asp Ser Thr Ala Thr Ile Val Asn Lys Leu Ile
350 355 360

Gln Ile Lys Ser Ser Asp Glu Arg Asn Thr Leu Met Ala Gly Leu
365 370 375

Pro Thr Tyr Pro Leu Gly Gly Thr Ser Ile Cys Ser Gly Ile Lys
380 385 390

Tyr Ala Phe Gln Val Ile Gly Glu Leu His Ser Gln Leu Asp Gly
395 400 405

Ser Glu Val Leu Leu Leu Thr Asp Gly Glu Asp Asn Thr Ala Ser
410 415 420

Ser Cys Ile Asp Glu Val Lys Gln Ser Gly Ala Ile Val His Phe
425 430 435

Ile Ala Leu Gly Arg Ala Ala Asp Glu Ala Val Ile Glu Met Ser
440 445 450

Lys Ile Thr Gly Gly Ser His Phe Tyr Val Ser Asp Glu Ala Gln
455 460 465

Asn Asn Gly Leu Ile Asp Ala Phe Gly Ala Leu Thr Ser Gly Asn
470 475 480

Thr Asp Leu Ser Gln Lys Ser Leu Gln Leu Glu Ser Lys Gly Leu
485 490 495

Thr Leu Asn Ser Asn Ala Trp Met Asn Asp Thr Val Ile Ile Asp
500 505 510

Ser Thr Val Gly Lys Asp Thr Phe Phe Leu Ile Thr Trp Asn Ser
515 520 525

Leu Pro Pro Ser Ile Ser Leu Trp Asp Pro Ser Gly Thr Ile Met
530 535 540

Glu Asn Phe Thr Val Asp Ala Thr Ser Lys Met Ala Tyr Leu Ser
545 550 555

Ile Pro Gly Thr Ala Lys Val Gly Thr Trp Ala Tyr Asn Leu Gln
560 565 570

Ala Lys Ala Asn Pro Glu Thr Leu Thr Ile Thr Val Thr Ser Arg
575 580 585

Ala Ala Asn Ser Ser Val Pro Pro Ile Thr Val Asn Ala Lys Met

590 595 600

Asn Lys Asp Val Asn Ser Phe Pro Ser Pro Met Ile Val Tyr Ala
605 610 615

Glu Ile Leu Gln Gly Tyr Val Pro Val Leu Gly Ala Asn Val Thr
620 625 630

Ala Phe Ile Glu Ser Gln Asn Gly His Thr Glu Val Leu Glu Leu
635 640 645

Leu Asp Asn Gly Ala Gly Ala Asp Ser Phe Lys Asn Asp Gly Val
650 655 660

Tyr Ser Arg Tyr Phe Thr Ala Tyr Thr Glu Asn Gly Arg Tyr Ser
665 670 675

Leu Lys Val Arg Ala His Gly Gly Ala Asn Thr Ala Arg Leu Lys
680 685 690

Leu Arg Pro Pro Leu Asn Arg Ala Ala Tyr Ile Pro Gly Trp Val
695 700 705

Val Asn Gly Glu Ile Glu Ala Asn Pro Pro Arg Pro Glu Ile Asp
710 715 720

Glu Asp Thr Gln Thr Thr Leu Glu Asp Phe Ser Arg Thr Ala Ser
725 730 735

Gly Gly Ala Phe Val Val Ser Gln Val Pro Ser Leu Pro Leu Pro
740 745 750

Asp Gln Tyr Pro Pro Ser Gln Ile Thr Asp Leu Asp Ala Thr Val
755 760 765

His Glu Asp Lys Ile Ile Leu Thr Trp Thr Ala Pro Gly Asp Asn
770 775 780

Phe Asp Val Gly Lys Val Gln Arg Tyr Ile Ile Arg Ile Ser Ala
785 790 795

Ser Ile Leu Asp Leu Arg Asp Ser Phe Asp Asp Ala Leu Gln Val
800 805 810

Asn Thr Thr Asp Leu Ser Pro Lys Glu Ala Asn Ser Lys Glu Ser
815 820 825

Phe Ala Phe Lys Pro Glu Asn Ile Ser Glu Glu Asn Ala Thr His
830 835 840

Ile Phe Ile Ala Ile Lys Ser Ile Asp Lys Ser Asn Leu Thr Ser
845 850 855

Lys Val Ser Asn Ile Ala Gln Val Thr Leu Phe Ile Pro Gln Ala
860 865 870

Asn Pro Asp Asp Ile Asp Pro Thr Pro Thr Pro Thr Pro Thr Pro
875 880 885

Thr Pro Asp Lys Ser His Asn Ser Gly Val Asn Ile Ser Thr Leu
890 895 900

Val Leu Ser Val Ile Gly Ser Val Val Ile Val Asn Phe Ile Leu

905 910 915

Ser Thr Thr Ile

<210> 380
<211> 3877
<212> DNA
<213> Homo sapiens

<400> 380
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gacccagagg agcaatgatg tagccacctc ctaaccttcc cttcttgaac 200

ccccagttat gccaggattt actagagagt gtcaactcaa ccagcaagcg 250

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aaggaaaggt cccctcttgc tgttggctgc acatcaggaa ggctgtgatg 400

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accccgagga gaagcctgtg aggaaggaca agcgggatga gttggtggaa 1200

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caatcaccgt ccttacacgg cctctgattt catagaaggg atctaccgaa 1300

cagaaaggga caaagggaca ttgtatgagc tcaccttcaa aggggaccac 1350

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gagaaaaata tatatatata tatatatatt gtgaaagatc aatccatctg 3450

ccagaatcta gtgggatgga agtttttgct acatgttatc caccccaggc 3500

caggtggaag taactgaatt atttttaaa ttaagcagtt ctactcaatc 3550

accaagatgc ttctgaaaat tgcattttat taccatttca aactattttt 3600

taaaaataaa tacagttaac atagagtggt ttcttcattc atgtgaaaat 3650

tattagccag caccagatgc atgagctaat tatctctttg agtccttgct 3700

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tgaaatttaa ttaaaacaca ggccatgaat ggaaggtggt attgcacagc 3850

taataaaata tgatttgtgg atatgaa 3877

<210> 381
<211> 532
<212> PRT
<213> Homo sapiens

<400> 381

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Val Val Leu Leu Val Leu Leu Cys Cys Ala Ile Ser Val Leu Tyr
                20                  25                  30

Met Leu Ala Cys Thr Pro Lys Gly Asp Glu Glu Gln Leu Ala Leu
                35                  40                  45

Pro Arg Ala Asn Ser Pro Thr Gly Lys Glu Gly Tyr Gln Ala Val
                50                  55                  60

Leu Gln Glu Trp Glu Glu Gln His Arg Asn Tyr Val Ser Ser Leu
                65                  70                  75

Lys Arg Gln Ile Ala Gln Leu Lys Glu Glu Leu Gln Glu Arg Ser
                80                  85                  90
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Glu Gln Leu Arg Asn Gly Gln Tyr Gln Ala Ser Asp Ala Ala Gly
95 100 105

Leu Gly Leu Asp Arg Ser Pro Pro Glu Lys Thr Gln Ala Asp Leu
110 115 120

Leu Ala Phe Leu His Ser Gln Val Asp Lys Ala Glu Val Asn Ala
125 130 135

Gly Val Lys Leu Ala Thr Glu Tyr Ala Ala Val Pro Phe Asp Ser
140 145 150

Phe Thr Leu Gln Lys Val Tyr Gln Leu Glu Thr Gly Leu Thr Arg
155 160 165

His Pro Glu Glu Lys Pro Val Arg Lys Asp Lys Arg Asp Glu Leu
170 175 180

Val Glu Ala Ile Glu Ser Ala Leu Glu Thr Leu Asn Asn Pro Ala
185 190 195

Glu Asn Ser Pro Asn His Arg Pro Tyr Thr Ala Ser Asp Phe Ile
200 205 210

Glu Gly Ile Tyr Arg Thr Glu Arg Asp Lys Gly Thr Leu Tyr Glu
215 220 225

Leu Thr Phe Lys Gly Asp His Lys His Glu Phe Lys Arg Leu Ile
230 235 240

Leu Phe Arg Pro Phe Ser Pro Ile Met Lys Val Lys Asn Glu Lys
245 250 255

Leu Asn Met Ala Asn Thr Leu Ile Asn Val Ile Val Pro Leu Ala
260 265 270

Lys Arg Val Asp Lys Phe Arg Gln Phe Met Gln Asn Phe Arg Glu
275 280 285

Met Cys Ile Glu Gln Asp Gly Arg Val His Leu Thr Val Val Tyr
290 295 300

Phe Gly Lys Glu Glu Ile Asn Glu Val Lys Gly Ile Leu Glu Asn
305 310 315

Thr Ser Lys Ala Ala Asn Phe Arg Asn Phe Thr Phe Ile Gln Leu
320 325 330

Asn Gly Glu Phe Ser Arg Gly Lys Gly Leu Asp Val Gly Ala Arg
335 340 345

Phe Trp Lys Gly Ser Asn Val Leu Leu Phe Phe Cys Asp Val Asp
350 355 360

Ile Tyr Phe Thr Ser Glu Phe Leu Asn Thr Cys Arg Leu Asn Thr
365 370 375

Gln Pro Gly Lys Lys Val Phe Tyr Pro Val Leu Phe Ser Gln Tyr
380 385 390

Asn Pro Gly Ile Ile Tyr Gly His His Asp Ala Val Pro Pro Leu
395 400 405

Glu Gln Gln Leu Val Ile Lys Lys Glu Thr Gly Phe Trp Arg Asp
410 415 420

Phe Gly Phe Gly Met Thr Cys Gln Tyr Arg Ser Asp Phe Ile Asn
425 430 435

Ile Gly Gly Phe Asp Leu Asp Ile Lys Gly Trp Gly Gly Glu Asp
440 445 450

Val His Leu Tyr Arg Lys Tyr Leu His Ser Asn Leu Ile Val Val
455 460 465

Arg Thr Pro Val Arg Gly Leu Phe His Leu Trp His Glu Lys Arg
470 475 480

Cys Met Asp Glu Leu Thr Pro Glu Gln Tyr Lys Met Cys Met Gln
485 490 495

Ser Lys Ala Met Asn Glu Ala Ser His Gly Gln Leu Gly Met Leu
500 505 510

Val Phe Arg His Glu Ile Glu Ala His Leu Arg Lys Gln Lys Gln
515 520 525

Lys Thr Ser Ser Lys Lys Thr
530

<210> 382
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 382
ctcggggaaa gggacttgat gttgg 25

<210> 383
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 383
gcgaaggtga gcctctatct cgtgcc 26

<210> 384
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 384
cagcctacac gtattgagg 19

<210> 385
<211> 48
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 385
cagtcagtac aatcctggca taatatacgg ccaccatgat gcagtccc 48

<210> 386
<211> 1346
<212> DNA
<213> Homo sapiens

<400> 386
gaaagaatgt tgtggctgct ctttttctg gtgactgcca ttcatgctga 50

actctgtcaa ccaggtgcag aaaatgcttt taaagtgaga cttagtatca 100

gaacagctct gggagataaa gcatatgcct gggataccaa tgaagaatac 150

ctcttcaaag cgatggtagc tttctccatg agaaaagttc ccaacagaga 200

agcaacagaa atttcccatg tcctactttg caatgtaacc cagagggtat 250

cattctggtt tgtggttaca gacccttcaa aaaatcacac ccttcctgct 300

gttgaggtgc aatcagccat aagaatgaac aagaaccgga tcaacaatgc 350

cttctttcta aatgaccaaa ctctggaatt tttaaaaatc ccttccacac 400

ttgcaccacc catggaccca tctgtgccca tctggattat tatatttggt 450

gtgatatttt gcatcatcat agttgcaatt gcactactga ttttatcagg 500

gatctggcaa cgtagaagaa agaacaaaga accatctgaa gtggatgacg 550

ctgaagataa gtgtgaaaac atgatcacaa ttgaaaatgg catcccctct 600

gatcccctgg acatgaaggg gggcatatta atgatgcctt catgacagag 650

gatgagaggc tcacccctct ctgaagggct gttgttctgc ttcctcaaga 700

aattaaacat ttgtttctgt gtgactgctg agcatcctga aataccaaga 750

gcagatcata tattttgttt caccattctt cttttgtaat aaattttgaa 800

tgtgcttgaa agtgaaaagc aatcaattat acccaccaac accactgaaa 850

tcataagcta ttcacgactc aaaatattct aaaatatttt tctgacagta 900

tagtgtataa atgtggtcat gtggtatttg tagttattga tttaagcatt 950

tttagaaata agatcaggca tatgtatata ttttcacact tcaaagacct 1000

aaggaaaaat aaattttcca gtggagaata catataatat ggtgtagaaa 1050

tcattgaaaa tggatccttt ttgacgatca cttatatcac tctgtatatg 1100

actaagtaaa caaaagtgag aagtaattat tgtaaatgga tggataaaaa 1150

tggaattact catatacagg gtggaatttt atcctgttat cacaccaaca 1200

gttgattata tattttctga atatcagccc ctaataggac aattctattt 1250

gttgaccatt tctacaattt gtaaaagtcc aatctgtgct aacttaataa 1300

agtaataatc atctcttttt aaaaaaaaaa aaaaaaaaaa aaaaaa 1346

<210> 387
<211> 212
<212> PRT
<213> Homo sapiens

<400> 387

Met	Leu	Trp	Leu	Leu	Phe	Phe	Leu	Val	Thr	Ala	Ile	His	Ala	Glu									
1				5					10					15									
Leu	Cys	Gln	Pro	Gly	Ala	Glu	Asn	Ala	Phe	Lys	Val	Arg	Leu	Ser									
				20					25					30									
Ile	Arg	Thr	Ala	Leu	Gly	Asp	Lys	Ala	Tyr	Ala	Trp	Asp	Thr	Asn									
				35					40					45									
Glu	Glu	Tyr	Leu	Phe	Lys	Ala	Met	Val	Ala	Phe	Ser	Met	Arg	Lys									
				50					55					60									
Val	Pro	Asn	Arg	Glu	Ala	Thr	Glu	Ile	Ser	His	Val	Leu	Leu	Cys									
				65					70					75									
Asn	Val	Thr	Gln	Arg	Val	Ser	Phe	Trp	Phe	Val	Val	Thr	Asp	Pro									
				80					85					90									
Ser	Lys	Asn	His	Thr	Leu	Pro	Ala	Val	Glu	Val	Gln	Ser	Ala	Ile									
				95					100					105									
Arg	Met	Asn	Lys	Asn	Arg	Ile	Asn	Asn	Ala	Phe	Phe	Leu	Asn	Asp									
				110					115					120									
Gln	Thr	Leu	Glu	Phe	Leu	Lys	Ile	Pro	Ser	Thr	Leu	Ala	Pro	Pro									
				125					130					135									
Met	Asp	Pro	Ser	Val	Pro	Ile	Trp	Ile	Ile	Ile	Phe	Gly	Val	Ile									
				140					145					150									
Phe	Cys	Ile	Ile	Ile	Val	Ala	Ile	Ala	Leu	Leu	Ile	Leu	Ser	Gly									
				155					160					165									
Ile	Trp	Gln	Arg	Arg	Arg	Lys	Asn	Lys	Glu	Pro	Ser	Glu	Val	Asp									
				170					175					180									
Asp	Ala	Glu	Asp	Lys	Cys	Glu	Asn	Met	Ile	Thr	Ile	Glu	Asn	Gly									
				185					190					195									
Ile	Pro	Ser	Asp	Pro	Leu	Asp	Met	Lys	Gly	Gly	Ile	Leu	Met	Met									
				200					205					210									
Pro	Ser																						

<210> 388
<211> 1371
<212> DNA
<213> Homo sapiens

<400> 388
aactcaaact cctctctctg ggaaaacgcg gtgcttgctc ctcccggagt 50

ggccttggca gggtgttgga gccctcggtc tgccccgtcc ggtctctggg 100

gccaaggctg ggtttccctc atgtatggca agagctctac tcgtgcggtg 150

cttcttctcc ttggcataca gctcacagct ctttggccta tagcagctgt 200

ggaaatttat acctcccggg tgctggaggc tgttaatggg acagatgctc 250

ggttaaaatg cactttctcc agctttgccc ctgtgggtga tgctctaaca 300

gtgacctgga attttcgtcc tctagacggg ggacctgagc agtttgtatt 350

ctactaccac atagatccct tccaacccat gagtgggcgg tttaaggacc 400

gggtgtcttg ggatgggaat cctgagcggt acgatgcctc catccttctc 450

tggaaactgc agttcgacga caatgggaca tacacctgcc aggtgaagaa 500

cccacctgat gttgatgggg tgatagggga gatccggctc agcgtcgtgc 550

acactgtacg cttctctgag atccacttcc tggctctggc cattggctct 600

gcctgtgcac tgatgatcat aatagtaatt gtagtggtcc tcttccagca 650

ttaccggaaa aagcgatggg ccgaaagagc tcataaagtg gtggagataa 700

aatcaaaaga agaggaaagg ctcaaccaag agaaaaaggt ctctgtttat 750

ttagaagaca cagactaaca attttagatg gaagctgaga tgatttccaa 800

gaacaagaac cctagtattt cttgaagtta atggaaactt ttctttggct 850

tttccagttg tgacccgttt tccaaccagt tctgcagcat attagattct 900

agacaagcaa caccctctg gagccagcac agtgctcctc catatcacca 950

gtcatacaca gcctcattat taaggtctta tttaatttca gagtgtaaat 1000

tttttcaagt gctcattagg ttttataaac aagaagctac atttttgccc 1050

ttaagacact acttacagtg ttatgacttg tatacacata tattggtatc 1100

aaaggggata aaagccaatt tgtctgttac atttcctttc acgtatttct 1150

tttagcagca cttctgctac taaagttaat gtgtttactc tctttccttc 1200

ccacattctc aattaaaagg tgagctaagc ctcctcggtg tttctgatta 1250

acagtaaatc ctaaattcaa actgttaaat gacattttta tttttatgtc 1300

tctccttaac tatgagacac atcttgtttt actgaatttc tttcaatatt 1350

ccaggtgata gatttttgtc g 1371

<210> 389
<211> 215
<212> PRT
<213> Homo sapiens

<400> 389
Met Tyr Gly Lys Ser Ser Thr Arg Ala Val Leu Leu Leu Gly
1 5 10 15

Ile Gln Leu Thr Ala Leu Trp Pro Ile Ala Ala Val Glu Ile Tyr
20 25 30

Thr Ser Arg Val Leu Glu Ala Val Asn Gly Thr Asp Ala Arg Leu
35 40 45

Lys Cys Thr Phe Ser Ser Phe Ala Pro Val Gly Asp Ala Leu Thr
50 55 60

Val Thr Trp Asn Phe Arg Pro Leu Asp Gly Gly Pro Glu Gln Phe
65 70 75

Val Phe Tyr Tyr His Ile Asp Pro Phe Gln Pro Met Ser Gly Arg
80 85 90

Phe Lys Asp Arg Val Ser Trp Asp Gly Asn Pro Glu Arg Tyr Asp
95 100 105

Ala Ser Ile Leu Leu Trp Lys Leu Gln Phe Asp Asp Asn Gly Thr
110 115 120

Tyr Thr Cys Gln Val Lys Asn Pro Pro Asp Val Asp Gly Val Ile
125 130 135

Gly Glu Ile Arg Leu Ser Val Val His Thr Val Arg Phe Ser Glu
140 145 150

Ile His Phe Leu Ala Leu Ala Ile Gly Ser Ala Cys Ala Leu Met
155 160 165

Ile Ile Ile Val Ile Val Val Val Leu Phe Gln His Tyr Arg Lys
170 175 180

Lys Arg Trp Ala Glu Arg Ala His Lys Val Val Glu Ile Lys Ser
185 190 195

Lys Glu Glu Glu Arg Leu Asn Gln Glu Lys Lys Val Ser Val Tyr
200 205 210

Leu Glu Asp Thr Asp
215

<210> 390
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 390
ccgaggccat ctagaggcca gagc 24

<210> 391
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 391
acaggcagag ccaatggcca gagc 24

<210> 392
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 392
gagaggactg cgggagtttg ggacctttgt gcagacgtgc tcatg 45

<210> 393
<211> 471
<212> DNA
<213> Homo sapiens

<400> 393
gcatttttgt ctgtgctccc tgatcttcag gtcaccacca tgaagttctt 50

agcagtcctg gtactcttgg gagtttccat ctttctggtc tctgcccaga 100

atccgacaac agctgctcca gctgacacgt atccagctac tggtcctgct 150

gatgatgaag cccctgatgc tgaaaccact gctgctgcaa ccactgcgac 200

cactgctgct cctaccactg caaccaccgc tgcttctacc actgctcgta 250

aagacattcc agttttaccc aaatgggttg gggatctccc gaatggtaga 300

gtgtgtccct gagatggaat cagcttgagt cttctgcaat tggtcacaac 350

tattcatgct tcctgtgatt tcatccaact acttaccttg cctacgatat 400

ccccttttatc tctaatcagt ttattttctt tcaaataaaa aataactatg 450

agcaacataa aaaaaaaaaa a 471

<210> 394
<211> 90
<212> PRT
<213> Homo sapiens

<400> 394
Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe
1 5 10 15

Leu Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr
20 25 30

Tyr Pro Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu
35 40 45

Thr Thr Ala Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr
50 55 60

Ala Thr Thr Ala Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val
65 70 75

Leu Pro Lys Trp Val Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
80 85 90

<210> 395
<211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 395
gctccctgat cttcatgtca ccacc 25

<210> 396
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 396
cagggacaca ctctaccatt cgggag 26

<210> 397
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 397
ccatctttct ggtctctgcc cagaatccga caacagctgc tc 42

<210> 398
<211> 907
<212> DNA
<213> Homo sapiens

<400> 398
ggactctgaa ggtcccaagc agctgctgag gcccccaagg aagtggttcc 50

aaccttggac ccctaggggt ctggatttgc tggttaacaa gataacctga 100

gggcaggacc ccatagggga atgctacctc ctgcccttcc acctgccctg 150

gtgttcacgg tggcctggtc cctccttgcc gagagagtgt cctgggtcag 200

ggacgcagag gacgctcaca gactccagcc ctttgttacc gagaggacac 250

ttggcaaggt ccagcgatgg tccggagtcc acacacagac tggcggcagg 300

gcaggagggg gacagttctg ttgtgcttgg ttggacagta agagggtctt 350

ggccagtcca gggtgggggg cggcaaactc cataaagaac cagagggtct 400

gggccccggc cacagagtca tctgcccagc tcctctgctg ctggccagtg 450

ggagtggcac gaggtggggc tttgtgccag taaaaccaca ggctggattt 500

gcctgcgggc catggtccct gtctagggca gcaattctca accttcttgc 550

tctcaggacc ccaaagagct ttcattgtat ctattgattt ttaccacatt 600

agcaattaaa actgagaaat gggccgggca cggtggctca cgcctgtaat 650

cccagcactt tgggaggccg aggcgggtgg atcacctgag atcaggagtt 700

caagaccagc ctggccaaca tggtgaaacc ttgtctacta aaaatacaaa 750

aaattagcca ggcacagtgg tgtgcactgg tagtcccagt tactcgggag 800

gctgaggcag gaaaatcgct tgaacccagg aggcggacgt tgcggtgagc 850

cgagatcgcg ccgctgattc cagcctgggc gacaagagtg agactccatc 900

tcacaca 907

<210> 399
<211> 120
<212> PRT
<213> Homo sapiens

<400> 399

Met	Leu	Pro	Pro	Ala	Leu	Pro	Pro	Ala	Leu	Val	Phe	Thr	Val	Ala	
1				5				10						15	
Trp	Ser	Leu	Leu	Ala	Glu	Arg	Val	Ser	Trp	Val	Arg	Asp	Ala	Glu	
				20				25						30	
Asp	Ala	His	Arg	Leu	Gln	Pro	Phe	Val	Thr	Glu	Arg	Thr	Leu	Gly	
				35				40						45	
Lys	Val	Gln	Arg	Trp	Ser	Gly	Val	His	Thr	Gln	Thr	Gly	Gly	Arg	
				50				55						60	
Ala	Gly	Gly	Gly	Gln	Phe	Cys	Cys	Ala	Trp	Leu	Asp	Ser	Lys	Arg	
				65				70						75	
Val	Leu	Ala	Ser	Pro	Gly	Trp	Gly	Ala	Ala	Asn	Ser	Ile	Lys	Asn	
				80				85						90	
Gln	Arg	Val	Trp	Ala	Pro	Ala	Thr	Glu	Ser	Ser	Ala	Gln	Leu	Leu	
				95				100						105	
Cys	Cys	Trp	Pro	Val	Gly	Val	Ala	Arg	Gly	Gly	Ala	Leu	Cys	Gln	
				110				115						120	

<210> 400
<211> 893
<212> DNA
<213> Homo sapiens

<400> 400
gtcatgccag tgcctgctct gtgcctgctc tgggccctgg caatggtgac 50

ccggcctgcc tcagcggccc ccatgggcgg cccagaactg gcacagcatg 100

aggagctgac cctgctcttc catgggaccc tgcagctggg ccaggccctc 150

aacggtgtgt acaggaccac ggagggacgg ctgacaaagg ccaggaacag 200

cctgggtctc tatggccgca caatagaact cctggggcag gaggtcagcc 250

ggggccggga tgcagcccag gaacttcggg caagcctgtt ggagactcag 300

atggaggagg atattctgca gctgcaggca gaggccacag ctgaggtgct 350

gggggaggtg gcccaggcac agaaggtgct acgggacagc gtgcagcggc 400

tagaagtcca gctgaggagc gcctggctgg gccctgccta ccgagaattt 450

gaggtcttaa aggctcacgc tgacaagcag agccacatcc tatgggccct 500

cacaggccac gtgcagcggc agaggcggga gatggtggca cagcagcatc 550

ggctgcgaca gatccaggag agactccaca cagcggcgct cccagcctga 600

atctgcctgg atggaactga ggaccaatca tgctgcaagg aacacttcca 650

cgccccgtga ggcccctgtg cagggaggag ctgcctgttc actgggatca 700

gccagggcgc cgggccccac ttctgagcac agagcagaga cagacgcagg 750

cggggacaaa ggcagaggat gtagccccat tggggagggg tggaggaagg 800

acatgtaccc tttcatgcct acacacccct cattaaagca gagtcgtggc 850

atttcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 893

<210> 401
<211> 198
<212> PRT
<213> Homo sapiens

<400> 401

Met	Pro	Val	Pro	Ala	Leu	Cys	Leu	Leu	Trp	Ala	Leu	Ala	Met	Val	
1				5					10						15
Thr	Arg	Pro	Ala	Ser	Ala	Ala	Pro	Met	Gly	Gly	Pro	Glu	Leu	Ala	
				20					25						30
Gln	His	Glu	Glu	Leu	Thr	Leu	Leu	Phe	His	Gly	Thr	Leu	Gln	Leu	
				35					40						45
Gly	Gln	Ala	Leu	Asn	Gly	Val	Tyr	Arg	Thr	Thr	Glu	Gly	Arg	Leu	
				50					55						60
Thr	Lys	Ala	Arg	Asn	Ser	Leu	Gly	Leu	Tyr	Gly	Arg	Thr	Ile	Glu	
				65					70						75
Leu	Leu	Gly	Gln	Glu	Val	Ser	Arg	Gly	Arg	Asp	Ala	Ala	Gln	Glu	
				80					85						90
Leu	Arg	Ala	Ser	Leu	Leu	Glu	Thr	Gln	Met	Glu	Glu	Asp	Ile	Leu	
				95					100						105
Gln	Leu	Gln	Ala	Glu	Ala	Thr	Ala	Glu	Val	Leu	Gly	Glu	Val	Ala	
				110					115						120
Gln	Ala	Gln	Lys	Val	Leu	Arg	Asp	Ser	Val	Gln	Arg	Leu	Glu	Val	
				125					130						135
Gln	Leu	Arg	Ser	Ala	Trp	Leu	Gly	Pro	Ala	Tyr	Arg	Glu	Phe	Glu	
				140					145						150
Val	Leu	Lys	Ala	His	Ala	Asp	Lys	Gln	Ser	His	Ile	Leu	Trp	Ala	
				155					160						165
Leu	Thr	Gly	His	Val	Gln	Arg	Gln	Arg	Arg	Glu	Met	Val	Ala	Gln	
				170					175						180
Gln	His	Arg	Leu	Arg	Gln	Ile	Gln	Glu	Arg	Leu	His	Thr	Ala	Ala	

185 190 195

Leu Pro Ala

<210> 402
<211> 1915
<212> DNA
<213> Homo sapiens

<400> 402
ggcaacatgg ctcagcaggc ttgccccaga gccatggcaa agaatggact 50

tgtaatttgc atcctggtga tcaccttact cctggaccag accaccagcc 100

acacatccag attaaaagcc aggaagcaca gcaaacgtcg agtgagagac 150

aaggatggag atctgaagac tcaaattgaa aagctctgga cagaagtcaa 200

tgccttgaag gaaattcaag ccctgcagac agtctgtctc cgaggcacta 250

aagttcacaa gaaatgctac cttgcttcag aaggtttgaa gcatttccat 300

gaggccaatg aagactgcat ttccaaagga ggaatcctgg ttatccccag 350

gaactccgac gaaatcaacg ccctccaaga ctatggtaaa aggagcctgc 400

caggtgtcaa tgacttttgg ctgggcatca atgacatggt cacggaaggc 450

aagtttgttg acgtcaacgg aatcgctatc tccttcctca actgggaccg 500

tgcacagcct aacggtggca agcgagaaaa ctgtgtcctg ttctcccaat 550

cagctcaggg caagtggagt gatgaggcct gtcgcagcag caagagatac 600

atatgcgagt tcaccatccc taaataggtc tttctccaat gtgtcctcca 650

agcaagattc atcataactt ataggttcat gatctctaag atcaagtaaa 700

aatcataatt tttacttatt aaaaaattgc aacacaagat caatgtccat 750

agcaatatga tagcatcagc caattttgct aacacatttc tttgggattt 800

tgcccttcct ggggtatagg ggatcagaaa tattgatcca tgtgcacgca 850

gataaaatgg cttctgctaa acagactaaa atctttctct ctagtctttc 900

tcacttgtac aaacccagtt tgttttcaaa aaatcacagt agcaatgcaa 950

ctcatcactc tagaaaagca agcttaggct acctgaaaga ttttcccttg 1000

gaagtttagc gtatgtttga ctaacaaaaa ttccctacat cagagactct 1050

aggtgctata taatccaaaa acttttcagc ctgttgctca ttctgtccca 1100

tgctggcaat aataccttgt cagcccatta cccttatttt gaattgctcc 1150

atctcctggt gggacttgta tcttgtctgc catatcagaa cacaaacccc 1200

tgaagaggtt ctgatttgat ttttttttt tcttcatgcc tacccttttt 1250

ttggaagttt ccagccgcaa tttgaaatga aatgacaagg tgtatatttg 1300

atcaattttc attcccacca ttgcattaca acctctaact taaatgggta 1350

accctaaggc atatcaaaga agcagattgc atgataaacg gaaatagaaa 1400

aaaagaacct acatttattt tgctttagca tccttactct caccttttat 1450

gagattgaga gtggacttac atttcctttt ttacattttc gtatatttat 1500

ttttttttagc catcattata tgtttaagtc tattatgggc aaccaatctt 1550

tggaagctga aaactgaatt taaagaatgc tatcttggaa aattgcatac 1600

gtctgtgcaa ttttttattc tgcctagtgc tattctgctt gtttaactag 1650

attgtacaaa ataacttcat tgcttaatat caaattacaa agtttagact 1700

tggagggaaa tgggcttttt agaagcaaac aattttaaat atattttgtt 1750

cttcaaataa atagtgttta aacattgaat gtgttttgtg aacaatatcc 1800

cactttgcaa actttaacta cacatgcttg gaattaagtt ttagctgttt 1850

tcattgctca ataataaagc ctgaattctg atcaataaaa aaaaaaaaaa 1900

aaaaaaaaaa aaaaa 1915

<210> 403
<211> 206
<212> PRT
<213> Homo sapiens

<400> 403

Met	Ala	Gln	Gln	Ala	Cys	Pro	Arg	Ala	Met	Ala	Lys	Asn	Gly	Leu		
1					5				10						15	
Val	Ile	Cys	Ile	Leu	Val	Ile	Thr	Leu	Leu	Leu	Asp	Gln	Thr	Thr		
					20				25						30	
Ser	His	Thr	Ser	Arg	Leu	Lys	Ala	Arg	Lys	His	Ser	Lys	Arg	Arg		
					35				40						45	
Val	Arg	Asp	Lys	Asp	Gly	Asp	Leu	Lys	Thr	Gln	Ile	Glu	Lys	Leu		
					50				55						60	
Trp	Thr	Glu	Val	Asn	Ala	Leu	Lys	Glu	Ile	Gln	Ala	Leu	Gln	Thr		
					65				70						75	
Val	Cys	Leu	Arg	Gly	Thr	Lys	Val	His	Lys	Lys	Cys	Tyr	Leu	Ala		
					80				85						90	
Ser	Glu	Gly	Leu	Lys	His	Phe	His	Glu	Ala	Asn	Glu	Asp	Cys	Ile		
					95				100						105	
Ser	Lys	Gly	Gly	Ile	Leu	Val	Ile	Pro	Arg	Asn	Ser	Asp	Glu	Ile		
					110				115						120	
Asn	Ala	Leu	Gln	Asp	Tyr	Gly	Lys	Arg	Ser	Leu	Pro	Gly	Val	Asn		
					125				130						135	
Asp	Phe	Trp	Leu	Gly	Ile	Asn	Asp	Met	Val	Thr	Glu	Gly	Lys	Phe		
					140				145						150	
Val	Asp	Val	Asn	Gly	Ile	Ala	Ile	Ser	Phe	Leu	Asn	Trp	Asp	Arg		

155 160 165

Ala Gln Pro Asn Gly Gly Lys Arg Glu Asn Cys Val Leu Phe Ser
170 175 180

Gln Ser Ala Gln Gly Lys Trp Ser Asp Glu Ala Cys Arg Ser Ser
185 190 195

Lys Arg Tyr Ile Cys Glu Phe Thr Ile Pro Lys
200 205

<210> 404
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 404
cctggttatc cccaggaact ccgac 25

<210> 405
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 405
ctcttgctgc tgcgacaggc ctc 23

<210> 406
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 406
cgccctccaa gactatggta aaaggagcct gccaggtgtc aatgac 46

<210> 407
<211> 570
<212> DNA
<213> Homo sapiens

<400> 407
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ggctctgcgt ggccctgtcc tgcagctccg ctgctgcttt cttagtgggc 150

tcggccaagc ctgtggccca gcctgtcgct gcgctggagt cggcggcgga 200

ggccggggcc gggaccctgg ccaacccccc cggcaccctc aacccgctga 250

agctcctgct gagcagcctg ggcatccccg tgaaccacct catagagggc 300

tcccagaagt gtgtggctga gctgggtccc caggccgtgg gggccgtgaa 350

ggccctgaag gccctgctgg gggccctgac agtgtttggc tgagccgaga 400

ctggagcatc tacacctgag gacaagacgc tgcccacccg cgagggctga 450

aaaccccgcc gcggggagga ccgtccatcc ccttcccccg gcccctctca 500

ataaacgtgg ttaagagcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 550

aaaaaaaaaa aaaaaaaaaa 570

<210> 408
<211> 104
<212> PRT
<213> Homo sapiens

<400> 408

Met	Lys	Leu	Ala	Ala	Leu	Leu	Gly	Leu	Cys	Val	Ala	Leu	Ser	Cys	
1				5				10						15	
Ser	Ser	Ala	Ala	Ala	Phe	Leu	Val	Gly	Ser	Ala	Lys	Pro	Val	Ala	
				20				25						30	
Gln	Pro	Val	Ala	Ala	Leu	Glu	Ser	Ala	Ala	Glu	Ala	Gly	Ala	Gly	
				35				40						45	
Thr	Leu	Ala	Asn	Pro	Leu	Gly	Thr	Leu	Asn	Pro	Leu	Lys	Leu	Leu	
				50				55						60	
Leu	Ser	Ser	Leu	Gly	Ile	Pro	Val	Asn	His	Leu	Ile	Glu	Gly	Ser	
				65				70						75	
Gln	Lys	Cys	Val	Ala	Glu	Leu	Gly	Pro	Gln	Ala	Val	Gly	Ala	Val	
				80				85						90	
Lys	Ala	Leu	Lys	Ala	Leu	Leu	Gly	Ala	Leu	Thr	Val	Phe	Gly		
				95				100							

<210> 409
<211> 2089
<212> DNA
<213> Homo sapiens

<400> 409
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aagggaggca ctccttggcc tccgcagccg atcacatgaa ggtggtgcca 100

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ggcccccagt cctcagtcgc cagagacccc agcccctcag aaccagacca 200

gcagggtagt gcaggctccc agggaggaag aggaagatga gcaggaggcc 250

agcgaggaga aggccggtga ggaagagaaa gcctggctga tggccagcag 300

gcagcagctt gccaaggaga cttcaaactt cggattcagc ctgctgcgaa 350

agatctccat gaggcacgat ggcaacatgg tcttctctcc atttggcatg 400

tccttggcca tgacaggctt gatgctgggg gccacagggc cgactgaaac 450

ccagatcaag agagggctcc acttgcaggc cctgaagccc accaagcccg 500

ggctcctgcc ttccctcttt aagggactca gagagaccct ctcccgcaac 550

ctggaactgg gcctctcaca ggggagtttt gccttcatcc acaaggattt 600

tgatgtcaaa gagactttct tcaatttatc caagaggtat tttgatacag 650

agtgcgtgcc tatgaatttt cgcaatgcct cacaggccaa aaggctcatg 700

aatcattaca ttaacaaaga gactcggggg aaaattccca aactgtttga 750

tgagattaat cctgaaacca aattaattct tgtggattac atcttgttca 800

aagggaaatg gttgacccca tttgaccctg tcttcaccga agtcgacact 850

ttccacctgg acaagtacaa gaccattaag gtgcccatga tgtacggtgc 900

aggcaagttt gcctccacct ttgacaagaa ttttcgttgt catgtcctca 950

aactgcccta ccaaggaaat gccaccatgc tggtggtcct catggagaaa 1000

atgggtgacc acctcgccct tgaagactac ctgaccacag acttggtgga 1050

gacatggctc agaaacatga aaaccagaaa catggaagtt ttctttccga 1100

agttcaagct agatcagaag tatgagatgc atgagctgct taggcagatg 1150

ggaatcagaa gaatcttctc acccttttgct gaccttagtg aactctcagc 1200

tactggaaga aatctccaag tatccagggt tttacgaaga acagtgattg 1250

aagttgatga aaggggcact gaggcagtgg caggaatctt gtcagaaatt 1300

actgcttatt ccatgcctcc tgtcatcaaa gtggaccggc catttcattt 1350

catgatctat gaagaaacct ctggaatgct tctgtttctg ggcagggtgg 1400

tgaatccgac tctcctataa ttcaggacat gcataagcac ttcgtgctgt 1450

agtagatgct gaatctgagg tatcaaacac acacaggata ccagcaatgg 1500

atggcagggg agagtgttcc ttttgttctt aactagttta gggtgttctc 1550

aaataaatac agtagtcccc acttatctga gggggataca ttcaaagacc 1600

cccagcagat gcctgaaacg gtggacagtg ctgaacctta tatatatttt 1650

ttcctacaca tacataccta tgataaagtt taatttataa attaggcaca 1700

gtaagagatt aacaataata acaacattaa gtaaaatgag ttacttgaac 1750

gcaagcactg caataccata acagtcaaac tgattataga gaaggctact 1800

aagtgactca tgggcgagga gcatagacag tgtggagaca ttgggcaagg 1850

ggagaattca catcctgggt gggacagagc aggacgatgc aagattccat 1900

cccactactc agaatggcat gctgcttaag acttttagat tgtttatttc 1950

tggaattttt catttaatgt ttttggacca tggttgacca tggttaactg 2000

agactgcaga aagcaaaacc atggataagg gaggactact acaaaagcat 2050

taaattgata catatttttt aaaaaaaaaa aaaaaaaaa 2089

<210> 410
<211> 444
<212> PRT
<213> Homo sapiens

<400> 410
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1 5 10 15

Val Trp Leu Val Pro Gly Leu Ala Pro Ser Pro Gln Ser Pro Glu
20 25 30

Thr Pro Ala Pro Gln Asn Gln Thr Ser Arg Val Val Gln Ala Pro
35 40 45

Arg Glu Glu Glu Glu Asp Glu Gln Glu Ala Ser Glu Glu Lys Ala
50 55 60

Gly Glu Glu Glu Lys Ala Trp Leu Met Ala Ser Arg Gln Gln Leu
65 70 75

Ala Lys Glu Thr Ser Asn Phe Gly Phe Ser Leu Leu Arg Lys Ile
80 85 90

Ser Met Arg His Asp Gly Asn Met Val Phe Ser Pro Phe Gly Met
95 100 105

Ser Leu Ala Met Thr Gly Leu Met Leu Gly Ala Thr Gly Pro Thr
110 115 120

Glu Thr Gln Ile Lys Arg Gly Leu His Leu Gln Ala Leu Lys Pro
125 130 135

Thr Lys Pro Gly Leu Leu Pro Ser Leu Phe Lys Gly Leu Arg Glu
140 145 150

Thr Leu Ser Arg Asn Leu Glu Leu Gly Leu Ser Gln Gly Ser Phe
155 160 165

Ala Phe Ile His Lys Asp Phe Asp Val Lys Glu Thr Phe Phe Asn
170 175 180

Leu Ser Lys Arg Tyr Phe Asp Thr Glu Cys Val Pro Met Asn Phe
185 190 195

Arg Asn Ala Ser Gln Ala Lys Arg Leu Met Asn His Tyr Ile Asn
200 205 210

Lys Glu Thr Arg Gly Lys Ile Pro Lys Leu Phe Asp Glu Ile Asn
215 220 225

Pro Glu Thr Lys Leu Ile Leu Val Asp Tyr Ile Leu Phe Lys Gly
230 235 240

Lys Trp Leu Thr Pro Phe Asp Pro Val Phe Thr Glu Val Asp Thr
245 250 255

Phe His Leu Asp Lys Tyr Lys Thr Ile Lys Val Pro Met Met Tyr
260 265 270

Gly Ala Gly Lys Phe Ala Ser Thr Phe Asp Lys Asn Phe Arg Cys
275 280 285

His Val Leu Lys Leu Pro Tyr Gln Gly Asn Ala Thr Met Leu Val
290 295 300

Val Leu Met Glu Lys Met Gly Asp His Leu Ala Leu Glu Asp Tyr
305 310 315

Leu Thr Thr Asp Leu Val Glu Thr Trp Leu Arg Asn Met Lys Thr
320 325 330

Arg Asn Met Glu Val Phe Phe Pro Lys Phe Lys Leu Asp Gln Lys
335 340 345

Tyr Glu Met His Glu Leu Leu Arg Gln Met Gly Ile Arg Arg Ile
350 355 360

Phe Ser Pro Phe Ala Asp Leu Ser Glu Leu Ser Ala Thr Gly Arg
365 370 375

Asn Leu Gln Val Ser Arg Val Leu Arg Arg Thr Val Ile Glu Val
380 385 390

Asp Glu Arg Gly Thr Glu Ala Val Ala Gly Ile Leu Ser Glu Ile
395 400 405

Thr Ala Tyr Ser Met Pro Pro Val Ile Lys Val Asp Arg Pro Phe
410 415 420

His Phe Met Ile Tyr Glu Glu Thr Ser Gly Met Leu Leu Phe Leu
425 430 435

Gly Arg Val Val Asn Pro Thr Leu Leu
440

<210> 411
<211> 636
<212> DNA
<213> Homo sapiens

<400> 411
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cccagacatg aggaggctcc tcctggtcac cagcctggtg gttgtgctgc 100

tgtgggaggc aggtgcagtc ccagcaccca aggtccctat caagatgcaa 150

gtcaaacact ggccctcaga gcaggaccca gagaaggcct ggggcgcccg 200

tgtggtggag cctccggaga aggacgacca gctggtggtg ctgttccctg 250

tccagaagcc gaaactcttg accaccgagg agaagccacg aggtcagggc 300

aggggcccca tccttccagg caccaaggcc tggatggaga ccgaggacac 350

cctgggccgt gtcctgagtc ccgagcccga ccatgacagc ctgtaccacc 400

ctccgcctga ggaggaccag ggcgaggaga ggccccggtt gtgggtgatg 450

ccaaatcacc aggtgctcct gggaccggag gaagaccaag accacatcta 500

ccacccccag tagggctcca ggggccatca ctgcccccgc cctgtcccaa 550

ggcccaggct gttgggactg ggaccctccc taccctgccc cagctagaca 600

aataaacccc agcaggcaaa aaaaaaaaaa aaaaaa 636

<210> 412
<211> 151
<212> PRT
<213> Homo sapiens

<400> 412

Met	Arg	Arg	Leu	Leu	Leu	Val	Thr	Ser	Leu	Val	Val	Val	Leu	Leu	
1				5				10						15	
Trp	Glu	Ala	Gly	Ala	Val	Pro	Ala	Pro	Lys	Val	Pro	Ile	Lys	Met	
				20				25						30	
Gln	Val	Lys	His	Trp	Pro	Ser	Glu	Gln	Asp	Pro	Glu	Lys	Ala	Trp	
				35				40						45	
Gly	Ala	Arg	Val	Val	Glu	Pro	Pro	Glu	Lys	Asp	Asp	Gln	Leu	Val	
				50				55						60	
Val	Leu	Phe	Pro	Val	Gln	Lys	Pro	Lys	Leu	Leu	Thr	Thr	Glu	Glu	
				65				70						75	
Lys	Pro	Arg	Gly	Gln	Gly	Arg	Gly	Pro	Ile	Leu	Pro	Gly	Thr	Lys	
				80				85						90	
Ala	Trp	Met	Glu	Thr	Glu	Asp	Thr	Leu	Gly	Arg	Val	Leu	Ser	Pro	
				95				100						105	
Glu	Pro	Asp	His	Asp	Ser	Leu	Tyr	His	Pro	Pro	Pro	Glu	Glu	Asp	
				110				115						120	
Gln	Gly	Glu	Glu	Arg	Pro	Arg	Leu	Trp	Val	Met	Pro	Asn	His	Gln	
				125				130						135	
Val	Leu	Leu	Gly	Pro	Glu	Glu	Asp	Gln	Asp	His	Ile	Tyr	His	Pro	
				140				145						150	

Gln

<210> 413
<211> 1176
<212> DNA
<213> Homo sapiens

<400> 413
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aggagctctc tgtacccaag gaaagtgcag ctgagactca gacaagatta 100

caatgaacca actcagcttc ctgctgtttc tcatagcgac caccagagga 150

tggagtacag atgaggctaa tacttacttc aaggaatgga cctgttcttc 200

gtctccatct ctgcccagaa gctgcaagga aatcaaagac gaatgtccta 250

gtgcatttga tggcctgtat tttctccgca ctgagaatgg tgttatctac 300

cagaccttct gtgacatgac ctctgggggt ggcggctgga ccctggtggc 350

cagcgtgcat gagaatgaca tgcgtgggaa gtgcacggtg ggcgatcgct 400

ggtccagtca gcagggcagc aaagcagact acccagaggg ggacggcaac 450

tgggccaact acaacacctt tggatctgca gaggcggcca cgagcgatga 500

ctacaagaac cctggctact acgacatcca ggccaaggac ctgggcatct 550

ggcacgtgcc caataagtcc cccatgcagc actggagaaa cagctccctg 600

ctgaggtacc gcacggacac tggcttcctc cagacactgg gacataatct 650

gtttggcatc taccagaaat atccagtgaa atatggagaa ggaaagtgtt 700

ggactgacaa cggcccggtg atccctgtgg tctatgattt tggcgacgcc 750

cagaaaacag catcttatta ctcaccctat ggccagcggg aattcactgc 800

gggatttgtt cagttcaggg tatttaataa cgagagagca gccaacgcct 850

tgtgtgctgg aatgagggtc accggatgta acactgagca tcactgcatt 900

ggtggaggag gatactttcc agaggccagt ccccagcagt gtggagattt 950

ttctggtttt gattggagtg gatatggaac tcatgttggt tacagcagca 1000

gccgtgagat aactgaggca gctgtgcttc tattctatcg ttgagagttt 1050

tgtgggaggg aacccagacc tctcctccca accatgagat cccaaggatg 1100

gagaacaact tacccagtag ctagaatgtt aatggcagaa gagaaaacaa 1150

taaatcatat tgactcaaga aaaaaa 1176

<210> 414
<211> 313
<212> PRT
<213> Homo sapiens

<400> 414

Met	Asn	Gln	Leu	Ser	Phe	Leu	Leu	Phe	Leu	Ile	Ala	Thr	Thr	Arg	
1				5				10						15	
Gly	Trp	Ser	Thr	Asp	Glu	Ala	Asn	Thr	Tyr	Phe	Lys	Glu	Trp	Thr	
				20				25						30	
Cys	Ser	Ser	Ser	Pro	Ser	Leu	Pro	Arg	Ser	Cys	Lys	Glu	Ile	Lys	
				35				40						45	
Asp	Glu	Cys	Pro	Ser	Ala	Phe	Asp	Gly	Leu	Tyr	Phe	Leu	Arg	Thr	
				50				55						60	
Glu	Asn	Gly	Val	Ile	Tyr	Gln	Thr	Phe	Cys	Asp	Met	Thr	Ser	Gly	
				65				70						75	
Gly	Gly	Gly	Trp	Thr	Leu	Val	Ala	Ser	Val	His	Glu	Asn	Asp	Met	
				80				85						90	
Arg	Gly	Lys	Cys	Thr	Val	Gly	Asp	Arg	Trp	Ser	Ser	Gln	Gln	Gly	
				95				100						105	
Ser	Lys	Ala	Asp	Tyr	Pro	Glu	Gly	Asp	Gly	Asn	Trp	Ala	Asn	Tyr	
				110				115						120	
Asn	Thr	Phe	Gly	Ser	Ala	Glu	Ala	Ala	Thr	Ser	Asp	Asp	Tyr	Lys	

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                125                 130                 135

Asn Pro Gly Tyr Tyr Asp Ile Gln Ala Lys Asp Leu Gly Ile Trp
                140                 145                 150

His Val Pro Asn Lys Ser Pro Met Gln His Trp Arg Asn Ser Ser
                155                 160                 165

Leu Leu Arg Tyr Arg Thr Asp Thr Gly Phe Leu Gln Thr Leu Gly
                170                 175                 180

His Asn Leu Phe Gly Ile Tyr Gln Lys Tyr Pro Val Lys Tyr Gly
                185                 190                 195

Glu Gly Lys Cys Trp Thr Asp Asn Gly Pro Val Ile Pro Val Val
                200                 205                 210

Tyr Asp Phe Gly Asp Ala Gln Lys Thr Ala Ser Tyr Tyr Ser Pro
                215                 220                 225

Tyr Gly Gln Arg Glu Phe Thr Ala Gly Phe Val Gln Phe Arg Val
                230                 235                 240

Phe Asn Asn Glu Arg Ala Ala Asn Ala Leu Cys Ala Gly Met Arg
                245                 250                 255

Val Thr Gly Cys Asn Thr Glu His His Cys Ile Gly Gly Gly Gly
                260                 265                 270

Tyr Phe Pro Glu Ala Ser Pro Gln Gln Cys Gly Asp Phe Ser Gly
                275                 280                 285

Phe Asp Trp Ser Gly Tyr Gly Thr His Val Gly Tyr Ser Ser Ser
                290                 295                 300

Arg Glu Ile Thr Glu Ala Ala Val Leu Leu Phe Tyr Arg
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<210> 415
<211> 1281
<212> DNA
<213> Homo sapiens

<400> 415
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tcggcgcgcg aggtgcttgg gccgcgctgc tcctggggac gctgcaggtg 150

ctagcgctgc tgggggccgc ccatgaaagc gcagccatgg cggcatctgc 200

aaacatagag aattctgggc ttccacacaa ctccagtgct aactcaacag 250

agactctcca acatgtgcct tctgaccata caaatgaaac ttccaacagt 300

actgtgaaac caccaacttc agttgcctca gactccagta atacaacggt 350

caccaccatg aaacctacag cggcatctaa tacaacaaca ccagggatgg 400

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ccacaatagt tcagtgacat ctgctgcttc atcagtaaca atcacaacaa 550

ctatgcattc tgaagcaaag aaaggatcaa aatttgatac tgggagcttt 600

gttggtggta ttgtattaac gctgggagtt ttatctattc tttacattgg 650

atgcaaaatg tattactcaa gaagaggcat tcggtatcga accatagatg 700

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attgatgctg ccctatcaat taattttggt ttattaatag tttaaaacaa 800

tattctcttt ttgaaaatag tataaacagg ccatgcatat aatgtacagt 850

gtattacgta aatatgtaaa gattcttcaa ggtaacaagg gtttgggttt 900

tgaaataaac atctggatct tatagaccgt tcatacaatg gttttagcaa 950

gttcatagta agacaaacaa gtcctatctt ttttttttgg ctggggtggg 1000

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tggatatatc ttaattacta atgccacaca gaaattatac aatcaaacta 1200

gatctgaagc ataatttaag aaaaacatca acatttttg tgctttaaac 1250

tgtagtagtt ggtctagaaa caaaatactc c 1281

<210> 416
<211> 208
<212> PRT
<213> Homo sapiens

<400> 416

Met	Gly	Leu	Gly	Ala	Arg	Gly	Ala	Trp	Ala	Ala	Leu	Leu	Leu	Gly	
1				5				10						15	
Thr	Leu	Gln	Val	Leu	Ala	Leu	Leu	Gly	Ala	Ala	His	Glu	Ser	Ala	
				20				25						30	
Ala	Met	Ala	Ala	Ser	Ala	Asn	Ile	Glu	Asn	Ser	Gly	Leu	Pro	His	
				35				40						45	
Asn	Ser	Ser	Ala	Asn	Ser	Thr	Glu	Thr	Leu	Gln	His	Val	Pro	Ser	
				50				55						60	
Asp	His	Thr	Asn	Glu	Thr	Ser	Asn	Ser	Thr	Val	Lys	Pro	Pro	Thr	
				65				70						75	
Ser	Val	Ala	Ser	Asp	Ser	Ser	Asn	Thr	Thr	Val	Thr	Thr	Met	Lys	
				80				85						90	
Pro	Thr	Ala	Ala	Ser	Asn	Thr	Thr	Thr	Pro	Gly	Met	Val	Ser	Thr	
				95				100						105	
Asn	Met	Thr	Ser	Thr	Thr	Leu	Lys	Ser	Thr	Pro	Lys	Thr	Thr	Ser	
				110				115						120	
Val	Ser	Gln	Asn	Thr	Ser	Gln	Ile	Ser	Thr	Ser	Thr	Met	Thr	Val	

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                125                 130                 135

Thr His Asn Ser Ser Val Thr Ser Ala Ala Ser Ser Val Thr Ile
                140                 145                 150

Thr Thr Thr Met His Ser Glu Ala Lys Lys Gly Ser Lys Phe Asp
                155                 160                 165

Thr Gly Ser Phe Val Gly Gly Ile Val Leu Thr Leu Gly Val Leu
                170                 175                 180

Ser Ile Leu Tyr Ile Gly Cys Lys Met Tyr Tyr Ser Arg Arg Gly
                185                 190                 195

Ile Arg Tyr Arg Thr Ile Asp Glu His Asp Ala Ile Ile
                200                 205
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<210> 417
<211> 1728
<212> DNA
<213> Homo sapiens

<400> 417

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gcgatggcga ccctgtgggg aggccttctt cggcttggct ccttgctcag 150

cctgtcgtgc ctggcgcttt ccgtgctgct gctggcgcag ctgtcagacg 200

ccgccaagaa tttcgaggat gtcagatgta aatgtatctg ccctccctat 250

aaagaaaatt ctgggcatat ttataataag aacatatctc agaaagattg 300

tgattgcctt catgttgtgg agcccatgcc tgtgcggggg cctgatgtag 350

aagcatactg tctacgctgt gaatgcaaat atgaagaaag aagctctgtc 400

acaatcaagg ttaccattat aatttatctc tccattttgg gccttctact 450

tctgtacatg gtatatctta ctctggttga gcccatactg aagaggcgcc 500

tctttggaca tgcacagttg atacagagtg atgatgatat tggggatcac 550

cagccttttg caaatgcaca cgatgtgcta gcccgctccc gcagtcgagc 600

caacgtgctg aacaaggtag aatatgcaca gcagcgctgg aagcttcaag 650

tccaagagca gcgaaagtct gtctttgacc ggcatgttgt cctcagctaa 700

ttgggaattg aattcaaggt gactagaaag aaacaggcag acaactggaa 750

agaactgact gggttttgct gggtttcatt ttaatacctt gttgatttca 800

ccaactgttg ctggaagatt caaaactgga agcaaaaact tgcttgattt 850

ttttttcttg ttaacgtaat aatagagaca tttttaaaag cacacagctc 900

aaagtcagcc aataagtctt ttcctatttg tgacttttac taataaaaat 950

aaatctgcct gtaaattatc ttgaagtcct ttacctggaa caagcactct 1000
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cttttttcacc acatagtttt aacttgactt tcaagataat tttcagggtt 1050

tttgttgttg ttgtttttttg tttgtttgtt ttggtgggag aggggaggga 1100

tgcctgggaa gtggttaaca actttttttca agtcacttta ctaaacaaac 1150

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agtgtagcca gcctcatcaa agagctgact tactcatttg acttttgcac 1250

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tgtgatgtct gatgcaatgc atcctagaac aaactggcca tttgctagtt 1400

tactctaaag actaaacata gtcttggtgt gtgtggtctt actcatcttc 1450

tagtaccttt aaggacaaat cctaaggact tggacacttg caataaagaa 1500

attttatttt aaacccaagc ctccctggat tgataatata tacacatttg 1550

tcagcatttc cggtcgtggt gagaggcagc tgtttgagct ccaatatgtg 1600

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ccattattgg ataactggct tttttcttcc tatgtcctct ttggaatgta 1700

acaataaaaa taatttttga aacatcaa 1728

<210> 418
<211> 198
<212> PRT
<213> Homo sapiens

<400> 418

Met	Ala	Thr	Leu	Trp	Gly	Gly	Leu	Leu	Arg	Leu	Gly	Ser	Leu	Leu	
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Ser	Leu	Ser	Cys	Leu	Ala	Leu	Ser	Val	Leu	Leu	Leu	Ala	Gln	Leu	
			20					25					30		
Ser	Asp	Ala	Ala	Lys	Asn	Phe	Glu	Asp	Val	Arg	Cys	Lys	Cys	Ile	
			35					40					45		
Cys	Pro	Pro	Tyr	Lys	Glu	Asn	Ser	Gly	His	Ile	Tyr	Asn	Lys	Asn	
			50					55					60		
Ile	Ser	Gln	Lys	Asp	Cys	Asp	Cys	Leu	His	Val	Val	Glu	Pro	Met	
			65					70					75		
Pro	Val	Arg	Gly	Pro	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Arg	Cys	Glu	
			80					85					90		
Cys	Lys	Tyr	Glu	Glu	Arg	Ser	Ser	Val	Thr	Ile	Lys	Val	Thr	Ile	
			95					100					105		
Ile	Ile	Tyr	Leu	Ser	Ile	Leu	Gly	Leu	Leu	Leu	Leu	Tyr	Met	Val	
			110					115					120		
Tyr	Leu	Thr	Leu	Val	Glu	Pro	Ile	Leu	Lys	Arg	Arg	Leu	Phe	Gly	
			125					130					135		

His Ala Gln Leu Ile Gln Ser Asp Asp Asp Ile Gly Asp His Gln
140 145 150

Pro Phe Ala Asn Ala His Asp Val Leu Ala Arg Ser Arg Ser Arg
155 160 165

Ala Asn Val Leu Asn Lys Val Glu Tyr Ala Gln Gln Arg Trp Lys
170 175 180

Leu Gln Val Gln Glu Gln Arg Lys Ser Val Phe Asp Arg His Val
185 190 195

Val Leu Ser

<210> 419
<211> 681
<212> DNA
<213> Homo sapiens

<400> 419
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gccttcctgt cccgcgggaa gcggcaggag ccgccgccga cacctgaagg 150

aaaattgggc cgatttccac ctatgatgca tcatcaccag gcaccctcag 200

atggccagac tcctggggct cgtttccaga ggtctcacct tgccgaggca 250

tttgcaaagg ccaaaggatc aggtggaggt gctggaggag gaggtagtgg 300

aagaggtctg atggggcaga ttattccaat ctacggtttt gggatttttt 350

tatatatact gtacattcta tttaaggtaa gtagaatcat cctaatcata 400

ttacatcaat gaaaatctaa tatggcgata aaaatcattg tctacattaa 450

aacttcttat agttcataaa attatttcaa atccatcatc tctttaaatc 500

ctgcctcctc ttcatgaggt acttaggata gccattattt cagtttcaca 550

taagaatgtt tactcaatgt ttaagtgttt tgccccaaaa ttcacaacta 600

acaaggcaga actaggactt gaacatggat cttttggttc ttaatccagt 650

gagtgataca attcaatgca ctcccctgcc a 681

<210> 420
<211> 128
<212> PRT
<213> Homo sapiens

<400> 420
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1 5 10 15

Val Leu Ala Leu Ser Leu Leu Leu Pro Lys Ala Phe Leu Ser Arg
20 25 30

Gly Lys Arg Gln Glu Pro Pro Pro Thr Pro Glu Gly Lys Leu Gly
35 40 45

Arg Phe Pro Pro Met Met His His His Gln Ala Pro Ser Asp Gly
50 55 60

Gln Thr Pro Gly Ala Arg Phe Gln Arg Ser His Leu Ala Glu Ala
65 70 75

Phe Ala Lys Ala Lys Gly Ser Gly Gly Gly Ala Gly Gly Gly Gly
80 85 90

Ser Gly Arg Gly Leu Met Gly Gln Ile Ile Pro Ile Tyr Gly Phe
95 100 105

Gly Ile Phe Leu Tyr Ile Leu Tyr Ile Leu Phe Lys Val Ser Arg
110 115 120

Ile Ile Leu Ile Ile Leu His Gln
125

<210> 421
<211> 1630
<212> DNA
<213> Homo sapiens

<400> 421
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gctcttcatc ttggatttga aagttgagag cagcatgttt tgcccactga 100

aactcatcct gctgccagtg ttactggatt attccttggg cctgaatgac 150

ttgaatgttt ccccgcctga gctaacagtc catgtgggtg attcagctct 200

gatgggatgt gttttccaga gcacagaaga caaatgtata ttcaagatag 250

actggactct gtcaccagga gagcacgcca aggacgaata tgtgctatac 300

tattactcca atctcagtgt gcctattggg cgcttccaga accgcgtaca 350

cttgatgggg gacatcttat gcaatgatgg ctctctcctg ctccaagatg 400

tgcaagaggc tgaccaggga acctatatct gtgaaatccg cctcaaaggg 450

gagagccagg tgttcaagaa ggcggtggta ctgcatgtgc ttccagagga 500

gcccaaagag ctcatggtcc atgtgggtgg attgattcag atgggatgtg 550

ttttccagag cacagaagtg aaacacgtga ccaaggtaga atggatattt 600

tcaggacggc gcgcaaagga ggagattgta tttcgttact accacaaact 650

caggatgtct gtggagtact cccagagctg gggccacttc cagaatcgtg 700

tgaacctggt gggggacatt ttccgcaatg acggttccat catgcttcaa 750

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gaacctggtg ttcaagaaaa ccattgtgct gcatgtcagc ccggaagagc 850

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aatcagttgg tgatcattgt gggaattgtc tgtgccacaa tcctgctgct 950

ccctgttctg atattgatcg tgaagaagac ctgtggaaat aagagttcag 1000

tgaattctac agtcttggtg aagaacacga agaagactaa tccagagata 1050

aaagaaaaac cctgccattt tgaaagatgt gaaggggaga aacacattta 1100

ctccccaata attgtacggg aggtgatcga ggaagaagaa ccaagtgaaa 1150

aatcagaggc cacctacatg accatgcacc cagtttggcc ttctctgagg 1200

tcagatcgga acaactcact tgaaaaaaag tcaggtgggg gaatgccaaa 1250

aacacagcaa gccttttgag aagaatggag agtcccttca tctcagcagc 1300

ggtggagact ctctcctgtg tgtgtcctgg gccactctac cagtgatttc 1350

agactcccgc tctcccagct gtcctcctgt ctcattgttt ggtcaataca 1400

ctgaagatgg agaatttgga gcctggcaga gagactggac agctctggag 1450

gaacaggcct gctgagggga ggggagcatg gacttggcct ctggagtggg 1500

acactggccc tgggaaccag gctgagctga gtggcctcaa acccccccgt 1550

ggatcagacc ctcctgtggg cagggttctt agtggatgag ttactgggaa 1600

gaatcagaga taaaaaccaa cccaaatcaa 1630

<210> 422
<211> 394
<212> PRT
<213> Homo sapiens

<400> 422

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				20				25						30	
Thr	Val	His	Val	Gly	Asp	Ser	Ala	Leu	Met	Gly	Cys	Val	Phe	Gln	
				35				40						45	
Ser	Thr	Glu	Asp	Lys	Cys	Ile	Phe	Lys	Ile	Asp	Trp	Thr	Leu	Ser	
				50				55						60	
Pro	Gly	Glu	His	Ala	Lys	Asp	Glu	Tyr	Val	Leu	Tyr	Tyr	Tyr	Ser	
				65				70						75	
Asn	Leu	Ser	Val	Pro	Ile	Gly	Arg	Phe	Gln	Asn	Arg	Val	His	Leu	
				80				85						90	
Met	Gly	Asp	Ile	Leu	Cys	Asn	Asp	Gly	Ser	Leu	Leu	Leu	Gln	Asp	
				95				100						105	
Val	Gln	Glu	Ala	Asp	Gln	Gly	Thr	Tyr	Ile	Cys	Glu	Ile	Arg	Leu	
				110				115						120	
Lys	Gly	Glu	Ser	Gln	Val	Phe	Lys	Lys	Ala	Val	Val	Leu	His	Val	
				125				130						135	
Leu	Pro	Glu	Glu	Pro	Lys	Glu	Leu	Met	Val	His	Val	Gly	Gly	Leu	
				140				145						150	
Ile	Gln	Met	Gly	Cys	Val	Phe	Gln	Ser	Thr	Glu	Val	Lys	His	Val	

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155 160 165

Thr Lys Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Glu Glu
170 175 180

Ile Val Phe Arg Tyr Tyr His Lys Leu Arg Met Ser Val Glu Tyr
185 190 195

Ser Gln Ser Trp Gly His Phe Gln Asn Arg Val Asn Leu Val Gly
200 205 210

Asp Ile Phe Arg Asn Asp Gly Ser Ile Met Leu Gln Gly Val Arg
215 220 225

Glu Ser Asp Gly Gly Asn Tyr Thr Cys Ser Ile His Leu Gly Asn
230 235 240

Leu Val Phe Lys Lys Thr Ile Val Leu His Val Ser Pro Glu Glu
245 250 255

Pro Arg Thr Leu Val Thr Pro Ala Ala Leu Arg Pro Leu Val Leu
260 265 270

Gly Gly Asn Gln Leu Val Ile Ile Val Gly Ile Val Cys Ala Thr
275 280 285

Ile Leu Leu Leu Pro Val Leu Ile Leu Ile Val Lys Lys Thr Cys
290 295 300

Gly Asn Lys Ser Ser Val Asn Ser Thr Val Leu Val Lys Asn Thr
305 310 315

Lys Lys Thr Asn Pro Glu Ile Lys Glu Lys Pro Cys His Phe Glu
320 325 330

Arg Cys Glu Gly Glu Lys His Ile Tyr Ser Pro Ile Ile Val Arg
335 340 345

Glu Val Ile Glu Glu Glu Glu Pro Ser Glu Lys Ser Glu Ala Thr
350 355 360

Tyr Met Thr Met His Pro Val Trp Pro Ser Leu Arg Ser Asp Arg
365 370 375

Asn Asn Ser Leu Glu Lys Lys Ser Gly Gly Gly Met Pro Lys Thr
380 385 390

Gln Gln Ala Phe

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<212> DNA
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ctctgagctc agttgcagta ctcgggaagc catgcaggat gaagatggat 200

acatcacctt aaatattaaa actcggaaac cagctctcgt ctccgttggc 250

cctgcatcct cctcctggtg gcgtgtgatg gctttgattc tgctgatcct 300

gtgcgtgggg atggttgtcg ggctggtggc tctggggatt tggtctgtca 350

tgcagcgcaa ttacctacaa gatgagaatg aaaatcgcac aggaactctg 400

caacaattag caaagcgctt ctgtcaatat gtggtaaaac aatcagaact 450

aaagggcact ttcaaaggtc ataaatgcag cccctgtgac acaaactgga 500

gatattatgg agatagctgc tatgggttct tcaggcacaa cttaacatgg 550

gaagagagta agcagtactg cactgacatg aatgctactc tcctgaagat 600

tgacaaccgg aacattgtgg agtacatcaa agccaggact catttaattc 650

gttgggtcgg attatctcgc cagaagtcga atgaggtctg gaagtgggag 700

gatggctcgg ttatctcaga aaatatgttt gagtttttgg aagatggaaa 750

aggaaatatg aattgtgctt attttcataa tgggaaaatg caccctacct 800

tctgtgagaa caaacattat ttaatgtgtg agaggaaggc tggcatgacc 850

aaggtggacc aactacctta atgcaaagag gtggacagga taacacagat 900

aagggcttta ttgtacaata aaagatatgt atgaatgcat cagtagctga 950

aaaaaaaaaa aaa 963

<210> 424
<211> 229
<212> PRT
<213> Homo sapiens

<400> 424

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Lys	Pro	Ala	Leu	Val	Ser	Val	Gly	Pro	Ala	Ser	Ser	Ser	Trp	Trp	
				20				25						30	
Arg	Val	Met	Ala	Leu	Ile	Leu	Leu	Ile	Leu	Cys	Val	Gly	Met	Val	
				35				40						45	
Val	Gly	Leu	Val	Ala	Leu	Gly	Ile	Trp	Ser	Val	Met	Gln	Arg	Asn	
				50				55						60	
Tyr	Leu	Gln	Asp	Glu	Asn	Glu	Asn	Arg	Thr	Gly	Thr	Leu	Gln	Gln	
				65				70						75	
Leu	Ala	Lys	Arg	Phe	Cys	Gln	Tyr	Val	Val	Lys	Gln	Ser	Glu	Leu	
				80				85						90	
Lys	Gly	Thr	Phe	Lys	Gly	His	Lys	Cys	Ser	Pro	Cys	Asp	Thr	Asn	
				95				100						105	
Trp	Arg	Tyr	Tyr	Gly	Asp	Ser	Cys	Tyr	Gly	Phe	Phe	Arg	His	Asn	
				110				115						120	
Leu	Thr	Trp	Glu	Glu	Ser	Lys	Gln	Tyr	Cys	Thr	Asp	Met	Asn	Ala	

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                125                 130                 135

Thr Leu Leu Lys Ile Asp Asn Arg Asn Ile Val Glu Tyr Ile Lys
                140                 145                 150

Ala Arg Thr His Leu Ile Arg Trp Val Gly Leu Ser Arg Gln Lys
                155                 160                 165

Ser Asn Glu Val Trp Lys Trp Glu Asp Gly Ser Val Ile Ser Glu
                170                 175                 180

Asn Met Phe Glu Phe Leu Glu Asp Gly Lys Gly Asn Met Asn Cys
                185                 190                 195

Ala Tyr Phe His Asn Gly Lys Met His Pro Thr Phe Cys Glu Asn
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Lys His Tyr Leu Met Cys Glu Arg Lys Ala Gly Met Thr Lys Val
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Asp Gln Leu Pro
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<210> 426
<211> 26
<212> DNA
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<220>
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<400> 426
ctgagataac cgagccatcc tcccac 26

<210> 427
<211> 49
<212> DNA
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<400> 427
gcttcctgac actaaggctg tctgctagtc agaattgcct caaaaagag 49

<210> 428
<211> 21
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<220>
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<400> 428
ccaccaatgg cagccccacc t 21

<210> 429
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<220>
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gactgccctc cctgcca 17

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caaaaagcct ggaagtcttc aaag 24

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<400> 431
cagctggact gcaggtgcta 20

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<220>
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cagtgagcac agcaagtgtc ct 22

<210> 433
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ggccacctcc ttgagtcttc agttccct 28

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caactactgg ctaaagctgg tgaa 24

<210> 435
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cctttctgta taggtgatac ccaatga 27

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tggccatccc taccagaggc aaaa 24

<210> 437
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<220>
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<400> 437
ctgaagacga cgcggattac ta 22

<210> 438
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<220>
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<400> 438
ggcagaaatg ggaggcaga 19

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<210> 446
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caggatacag tgggaatctt gaga 24

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<400> 448
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<210> 449
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<220>
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<210> 450
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<400> 450
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<210> 451
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<220>
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<400> 451
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<210> 452
<211> 24
<212> DNA
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aacgtgctac acgaccagtg tact 24

<210> 453
<211> 27
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 453
cacagcatat tcagatgact aaatcca 27

<210> 454
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 454
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<210> 455
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 455
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<210> 456
<211> 20
<212> DNA
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<220>
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tgatgtgcct ggctcagaac 20

<210> 457
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<212> DNA
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<220>
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<400> 457
tgcacctaga tgtccccagc accc 24

<210> 458
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<212> DNA
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aagatgcgcc aggcttctta 20

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<400> 461
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<210> 462
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<220>
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<400> 462
caaattaaag tacccatcag gagagaa 27

<210> 463
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<212> DNA
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<400> 463
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<210> 464
<211> 20
<212> DNA
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<220>
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<400> 464
gtgctgccca caattcatga 20

<210> 465
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
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<400> 465
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<210> 466
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<210> 467
<211> 22
<212> DNA
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<220>
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ctgaggaacc agccatgtct ct 22

<210> 468
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<400> 468
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<220>
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<210> 470
<211> 22
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<400> 470
gggtggaggc tcactgagta ga 22

<210> 471
<211> 28
<212> DNA
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<220>
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<400> 471
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<210> 474
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<210> 475
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<220>
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<400> 475
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<212> DNA
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<220>
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<400> 476
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<210> 477
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<220>
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<210> 478
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<400> 479
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<210> 480
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 487
catgattggt cctcagttcc atc 23

<210> 488
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 488
atagagggct cccagaagtg 20

<210> 489
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 489
cagggccttc agggccttca c 21

<210> 490
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 490
gctcagccaa acactgtca 19

<210> 491
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 491
ggggccctga cagtgtt 17

<210> 492
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 492
ctgagccgag actggagcat ctacac 26

<210> 493
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 493
gtgggcagcg tcttgtc 17

<210> 494
<211> 1231
<212> DNA
<213> Homo Sapien

<400> 494
cccacgcgtc cgcgcagtcg cgcagttctg cctccgcctg ccagtctcgc 50

ccgcgatccc ggcccggggc tgtggcgtcg actccgaccc aggcagccag 100

cagcccgcgc gggagccgga ccgccgccgg aggagctcgg acggcatgct 150

gagccccctc ctttgctgaa gcccgagtgc ggagaagccc gggcaaacgc 200

aggctaagga gaccaaagcg gcgaagtcgc gagacagcgg acaagcagcg 250

gaggagaagg aggaggaggc gaacccagag aggggcagca aaagaagcgg 300

tggtggtggg cgtcgtggcc atggcggcgg ctatcgccag ctcgctcatc 350

cgtcagaaga ggcaagcccg cgagcgcgag aaatccaacg cctgcaagtg 400

tgtcagcagc cccagcaaag gcaagaccag ctgcgacaaa aacaagttaa 450

atgtcttttc ccgggtcaaa ctcttcggct ccaagaagag gcgcagaaga 500

agaccagagc ctcagcttaa gggtatagtt accaagctat acagccgaca 550

aggctaccac ttgcagctgc aggcggatgg aaccattgat ggcaccaaag 600

atgaggacag cacttacact ctgtttaacc tcatccctgt gggtctgcga 650

gtggtggcta tccaaggagt tcaaaccaag ctgtacttgg caatgaacag 700

tgagggatac ttgtacacct cggaactttt cacacctgag tgcaaattca 750

aagaatcagt gtttgaaaat tattatgtga catattcatc aatgatatac 800

cgtcagcagc agtcaggccg agggtggtat ctgggtctga acaaagaagg 850

agagatcatg aaaggcaacc atgtgaagaa gaacaagcct gcagctcatt 900

ttctgcctaa accactgaaa gtggccatgt acaaggagcc atcactgcac 950

gatctcacgg agttctcccg atctggaagc gggaccccaa ccaagagcag 1000

aagtgtctct ggcgtgctga acggaggcaa atccatgagc cacaatgaat 1050

caacgtagcc agtgagggca aaagaagggc tctgtaacag aaccttacct 1100

ccaggtgctg ttgaattctt ctagcagtcc ttcacccaaa agttcaaatt 1150

tgtcagtgac atttaccaaa caaacaggca gagttcacta ttctatctgc 1200

cattagacct tcttatcatc catactaaag c 1231

<210> 495
<211> 245
<212> PRT
<213> Homo Sapien

<400> 495

Met	Ala	Ala	Ala	Ile	Ala	Ser	Ser	Leu	Ile	Arg	Gln	Lys	Arg	Gln	
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Ala	Arg	Glu	Arg	Glu	Lys	Ser	Asn	Ala	Cys	Lys	Cys	Val	Ser	Ser	
				20					25					30	
Pro	Ser	Lys	Gly	Lys	Thr	Ser	Cys	Asp	Lys	Asn	Lys	Leu	Asn	Val	
				35					40					45	
Phe	Ser	Arg	Val	Lys	Leu	Phe	Gly	Ser	Lys	Lys	Arg	Arg	Arg	Arg	
				50					55					60	
Arg	Pro	Glu	Pro	Gln	Leu	Lys	Gly	Ile	Val	Thr	Lys	Leu	Tyr	Ser	
				65					70					75	
Arg	Gln	Gly	Tyr	His	Leu	Gln	Leu	Gln	Ala	Asp	Gly	Thr	Ile	Asp	
				80					85					90	
Gly	Thr	Lys	Asp	Glu	Asp	Ser	Thr	Tyr	Thr	Leu	Phe	Asn	Leu	Ile	
				95					100					105	
Pro	Val	Gly	Leu	Arg	Val	Val	Ala	Ile	Gln	Gly	Val	Gln	Thr	Lys	
				110					115					120	
Leu	Tyr	Leu	Ala	Met	Asn	Ser	Glu	Gly	Tyr	Leu	Tyr	Thr	Ser	Glu	
				125					130					135	
Leu	Phe	Thr	Pro	Glu	Cys	Lys	Phe	Lys	Glu	Ser	Val	Phe	Glu	Asn	
				140					145					150	
Tyr	Tyr	Val	Thr	Tyr	Ser	Ser	Met	Ile	Tyr	Arg	Gln	Gln	Gln	Ser	
				155					160					165	
Gly	Arg	Gly	Trp	Tyr	Leu	Gly	Leu	Asn	Lys	Glu	Gly	Glu	Ile	Met	
				170					175					180	
Lys	Gly	Asn	His	Val	Lys	Lys	Asn	Lys	Pro	Ala	Ala	His	Phe	Leu	
				185					190					195	
Pro	Lys	Pro	Leu	Lys	Val	Ala	Met	Tyr	Lys	Glu	Pro	Ser	Leu	His	
				200					205					210	
Asp	Leu	Thr	Glu	Phe	Ser	Arg	Ser	Gly	Ser	Gly	Thr	Pro	Thr	Lys	

215 220 225

Ser Arg Ser Val Ser Gly Val Leu Asn Gly Gly Lys Ser Met Ser
230 235 240

His Asn Glu Ser Thr
245

<210> 496
<211> 1471
<212> DNA
<213> Homo Sapien

<400> 496
ccaggatgga gctggggcct gtatagccat attattgttc tatgctacta 50

gacatggggg ggacttggtg aaaaaggtat tatccagcca gagggtctgg 100

gagccctgtc ttactgaacc tgggcaacct ggatattctg agacatattt 150

tgggggggatt tcagtgaaaa aagtggggga tcccctccat ttagagtgta 200

gcaaaggaaa aaacaccaag gttgggttcc ttcctgacat tggcagtgcc 250

ccagtagggg tgggatgagc gaatattccc aaagctaaag tcccacaccc 300

tgtagattac aagagtggat ttggcaggag tgtgccccaa aatacagtgg 350

aaaggtgcct gaagatattt aaaccacgtc ttggaaattt agtgggtctt 400

ggctttggga taggtgaagt gaggacagac actggagagg agggaaaggg 450

gacgttttca ataggaggca aaactcgagg gtgggatcca ctgaggagta 500

cataggctgc tggatctggt ggagccagca ctgggcccac gggtggtaac 550

tggctgctgt ggaggggggt acgtgagggg ggggtctggg gcttatcctc 600

aggtcctgtg ggtggggcag cgagtcgggg cctgagcgtc aagagcatgc 650

cctagtgagc gggctcctct gggggagccc agcgcgctcc gggcgcctgc 700

cggtttgggg gtgtctcctc ccggggcgct atggcggcgc tggccagtag 750

cctgatccgg cagaagcggg aggtccgcga gcccgggggc agccggccgg 800

tgtcggcgca gcggcgcgtg tgtccccgcg gcaccaagtc cctttgccag 850

aagcagctcc tcatcctgct gtccaaggtg cgactgtgcg gggggcggcc 900

cgcgcggccg gaccgcggcc cggagcctca gctcaaaggc atcgtcacca 950

aactgttctg ccgccagggt ttctacctcc aggcgaatcc cgacggaagc 1000

atccagggca ccccagagga taccagctcc ttcacccact tcaacctgat 1050

ccctgtgggc ctccgtgtgg tcaccatcca gagcgccaag ctgggtcact 1100

acatggccat gaatgctgag ggactgctct acagttcgcc gcatttcaca 1150

gctgagtgtc gctttaagga gtgtgtcttt gagaattact acgtcctgta 1200

cgcctctgct ctctaccgcc agcgtcgttc tggccgggcc tggtacctcg 1250

Replacement Sheet

gcctggacaa ggagggccag gtcatgaagg gaaaccgagt taagaagacc 1300

aaggcagctg cccactttct gcccaagctc ctggaggtgg ccatgtacca 1350

ggagccttct ctccacagtg tccccgaggc ctccccttcc agtccccctg 1400

ccccctgaaa tgtagtccct ggactggagg ttccctgcac tcccagtgag 1450

ccagccacca ccacaacctg t 1471

<210> 497
<211> 225
<212> PRT
<213> Homo Sapien

<400> 497

Met	Ala	Ala	Leu	Ala	Ser	Ser	Leu	Ile	Arg	Gln	Lys	Arg	Glu	Val	
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Arg	Glu	Pro	Gly	Gly	Ser	Arg	Pro	Val	Ser	Ala	Gln	Arg	Arg	Val	
				20				25						30	
Cys	Pro	Arg	Gly	Thr	Lys	Ser	Leu	Cys	Gln	Lys	Gln	Leu	Leu	Ile	
				35				40						45	
Leu	Leu	Ser	Lys	Val	Arg	Leu	Cys	Gly	Gly	Arg	Pro	Ala	Arg	Pro	
				50				55						60	
Asp	Arg	Gly	Pro	Glu	Pro	Gln	Leu	Lys	Gly	Ile	Val	Thr	Lys	Leu	
				65				70						75	
Phe	Cys	Arg	Gln	Gly	Phe	Tyr	Leu	Gln	Ala	Asn	Pro	Asp	Gly	Ser	
				80				85						90	
Ile	Gln	Gly	Thr	Pro	Glu	Asp	Thr	Ser	Ser	Phe	Thr	His	Phe	Asn	
				95				100						105	
Leu	Ile	Pro	Val	Gly	Leu	Arg	Val	Val	Thr	Ile	Gln	Ser	Ala	Lys	
				110				115						120	
Leu	Gly	His	Tyr	Met	Ala	Met	Asn	Ala	Glu	Gly	Leu	Leu	Tyr	Ser	
				125				130						135	
Ser	Pro	His	Phe	Thr	Ala	Glu	Cys	Arg	Phe	Lys	Glu	Cys	Val	Phe	
				140				145						150	
Glu	Asn	Tyr	Tyr	Val	Leu	Tyr	Ala	Ser	Ala	Leu	Tyr	Arg	Gln	Arg	
				155				160						165	
Arg	Ser	Gly	Arg	Ala	Trp	Tyr	Leu	Gly	Leu	Asp	Lys	Glu	Gly	Gln	
				170				175						180	
Val	Met	Lys	Gly	Asn	Arg	Val	Lys	Lys	Thr	Lys	Ala	Ala	Ala	His	
				185				190						195	
Phe	Leu	Pro	Lys	Leu	Leu	Glu	Val	Ala	Met	Tyr	Gln	Glu	Pro	Ser	
				200				205						210	
Leu	His	Ser	Val	Pro	Glu	Ala	Ser	Pro	Ser	Ser	Pro	Pro	Ala	Pro	
				215				220						225	

<210> 498
<211> 744

<212> DNA
<213> Homo Sapien

<400> 498
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ggagcagcac tgggaccggc cgtctgccag caggaggcgg agcagcccca 100

gcaagaaccg cgggctctgc aacggcaacc tggtggatat cttctccaaa 150

gtgcgcatct tcggcctcaa gaagcgcagg ttgcggcgcc aagatcccca 200

gctcaagggt atagtgacca ggttatattg caggcaaggc tactacttgc 250

aaatgcaccc cgatggagct ctcgatggaa ccaaggatga cagcactaat 300

tctacactct tcaacctcat accagtggga ctacgtgttg ttgccatcca 350

gggagtgaaa acagggttgt atatagccat gaatggagaa ggttacctct 400

acccatcaga acttttacc cctgaatgca agtttaaaga atctgttttt 450

gaaaattatt atgtaatcta ctcatccatg ttgtacagac aacaggaatc 500

tggtagagcc tggtttttgg gattaaataa ggaagggcaa gctatgaaag 550

ggaacagagt aaagaaaacc aaaccagcag ctcattttct acccaagcca 600

ttggaagttg ccatgtaccg agaaccatct ttgcatgatg ttggggaaac 650

ggtcccgaag cctggggtga cgccaagtaa aagcacaagt gcgtctgcaa 700

taatgaatgg aggcaaacca gtcaacaaga gtaagacaac atag 744

<210> 499
<211> 247
<212> PRT
<213> Homo Sapien

<400> 499
Met Ala Ala Ala Ile Ala Ser Gly Leu Ile Arg Gln Lys Arg Gln
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Ala Arg Glu Gln His Trp Asp Arg Pro Ser Ala Ser Arg Arg Arg
20 25 30

Ser Ser Pro Ser Lys Asn Arg Gly Leu Cys Asn Gly Asn Leu Val
35 40 45

Asp Ile Phe Ser Lys Val Arg Ile Phe Gly Leu Lys Lys Arg Arg
50 55 60

Leu Arg Arg Gln Asp Pro Gln Leu Lys Gly Ile Val Thr Arg Leu
65 70 75

Tyr Cys Arg Gln Gly Tyr Tyr Leu Gln Met His Pro Asp Gly Ala
80 85 90

Leu Asp Gly Thr Lys Asp Asp Ser Thr Asn Ser Thr Leu Phe Asn
95 100 105

Leu Ile Pro Val Gly Leu Arg Val Val Ala Ile Gln Gly Val Lys
110 115 120

Thr Gly Leu Tyr Ile Ala Met Asn Gly Glu Gly Tyr Leu Tyr Pro
125 130 135

Ser Glu Leu Phe Thr Pro Glu Cys Lys Phe Lys Glu Ser Val Phe
140 145 150

Glu Asn Tyr Tyr Val Ile Tyr Ser Ser Met Leu Tyr Arg Gln Gln
155 160 165

Glu Ser Gly Arg Ala Trp Phe Leu Gly Leu Asn Lys Glu Gly Gln
170 175 180

Ala Met Lys Gly Asn Arg Val Lys Lys Thr Lys Pro Ala Ala His
185 190 195

Phe Leu Pro Lys Pro Leu Glu Val Ala Met Tyr Arg Glu Pro Ser
200 205 210

Leu His Asp Val Gly Glu Thr Val Pro Lys Pro Gly Val Thr Pro
215 220 225

Ser Lys Ser Thr Ser Ala Ser Ala Ile Met Asn Gly Gly Lys Pro
230 235 240

Val Asn Lys Ser Lys Thr Thr
245

<210> 500
<211> 2906
<212> DNA
<213> Homo Sapien

<400> 500
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ggctgttggg tgccttgcaa aaatgaagga tgcaggacgc agctttctcc 100

tggaaccgaa cgcaatggat aaactgattg tgcaagagag aaggaagaac 150

gaagcttttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200

acacagggag cattcaagaa tgaaataaac cagagttaga cccgcggggg 250

ttggtgtgtt ctgacataaa taaataatct taaagcagct gttcccctcc 300

ccacccccaa aaaaaaggat gattggaaat gaagaaccga ggattcacaa 350

agaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400

gatatttttg gaatgaaaag tttggggctt ttttagtaaa gtaaagaact 450

ggtgtggtgg tgttttcctt tctttttgaa tttcccacaa gaggagagga 500

aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgcg 550

gcagattgag gcattgattg ggggagagaa accagcagag cacagttgga 600

tttgtgccta tgttgactaa aattgacgga taattgcagt tggatttttc 650

ttcatcaacc tccttttttt taaattttta ttccttttgg tatcaagatc 700

atgcgttttc tcttgttctt aaccacctgg atttccatct ggatgttgct 750

gtgatcagtc tgaaatacaa ctgtttgaat tccagaagga ccaacaccag 800

ataaattatg aatgttgaac aagatgacct tacatccaca gcagataatg 850

ataggtccta ggtttaacag ggccctattt gacccccctgc ttgtggtgct 900

gctggctctt caacttcttg tggtggctgg tctggtgcgg gctcagacct 950

gcccttctgt gtgctcctgc agcaaccagt tcagcaaggt gatttgtgtt 1000

cggaaaaacc tgcgtgaggt tccggatggc atctccacca acacacggct 1050

gctgaacctc catgagaacc aaatccagat catcaaagtg aacagcttca 1100

agcacttgag gcacttggaa atcctacagt tgagtaggaa ccatatcaga 1150

accattgaaa ttggggcttt caatggtctg gcgaacctca acactctgga 1200

actctttgac aatcgtctta ctaccatccc gaatggagct tttgtatact 1250

tgtctaaact gaaggagctc tggttgcgaa acaaccccat tgaaagcatc 1300

ccttcttatg cttttaacag aattccttct ttgcgccgac tagacttagg 1350

ggaattgaaa agactttcat acatctcaga aggtgccttt gaaggtctgt 1400

ccaacttgag gtatttgaac cttgccatgt gcaaccttcg ggaaatccct 1450

aacctcacac cgctcataaa actagatgag ctggatcttt ctgggaatca 1500

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gacaaccttc agtcactagt ggagatcaac ctggcacaca ataatctaac 1650

attactgcct catgacctct tcactccctt gcatcatcta gagcggatac 1700

atttacatca caacccttgg aactgtaact gtgacatact gtggctcagc 1750

tggtggataa aagacatggc cccctcgaac acagcttgtt gtgcccggtg 1800

taacactcct cccaatctaa aggggaggta cattggagag ctcgaccaga 1850

attacttcac atgctatgct ccggtgattg tggagccccc tgcagacctc 1900

aatgtcactg aaggcatggc agctgagctg aaatgtcggg cctccacatc 1950

cctgacatct gtatcttgga ttactccaaa tggaacagtc atgacacatg 2000

gggcgtacaa agtgcggata gctgtgctca gtgatggtac gttaaatttc 2050

acaaatgtaa ctgtgcaaga tacaggcatg tacacatgta tggtgagtaa 2100

ttccgttggg aatactactg cttcagccac cctgaatgtt actgcagcaa 2150

ccactactcc tttctcttac ttttcaaccg tcacagtaga gactatggaa 2200

ccgtctcagg atgaggcacg gaccacagat aacaatgtgg gtcccactcc 2250

agtggtcgac tgggagacca ccaatgtgac cacctctctc acaccacaga 2300

gcacaaggtc gacagagaaa accttcacca tcccagtgac tgatataaac 2350

agtgggatcc caggaattga tgaggtcatg aagactacca aaatcatcat 2400

tgggtgtttt gtggccatca cactcatggc tgcagtgatg ctggtcattt 2450

tctacaagat gaggaagcag caccatcggc aaaaccatca cgccccaaca 2500

aggactgttg aaattattaa tgtggatgat gagattacgg gagacacacc 2550

catggaaagc cacctgccca tgcctgctat cgagcatgag cacctaaatc 2600

actataactc atacaaatct cccttcaacc acacaacaac agttaacaca 2650

ataaattcaa tacacagttc agtgcatgaa ccgttattga tccgaatgaa 2700

ctctaaagac aatgtacaag agactcaaat ctaaaacatt tacagagtta 2750

caaaaaacaa acaatcaaaa aaaaagacag tttattaaaa atgacacaaa 2800

tgactgggct aaatctactg tttcaaaaaa gtgtctttac aaaaaaacaa 2850

aaaagaaaag aaatttattt attaaaaatt ctattgtgat ctaaagcaga 2900

caaaaa 2906

<210> 501
<211> 640
<212> PRT
<213> Homo Sapien

<400> 501

Met Leu Asn Lys Met Thr Leu His Pro Gln Gln Ile Met Ile Gly
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Pro Arg Phe Asn Arg Ala Leu Phe Asp Pro Leu Leu Val Val Leu
20 25 30

Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln
35 40 45

Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val
50 55 60

Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser
65 70 75

Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile
80 85 90

Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu
95 100 105

Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe
110 115 120

Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg
125 130 135

Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu
140 145 150

Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser
155 160 165

Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly
170 175 180

Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly
185 190 195

Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg
200 205 210

Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp
215 220 225

Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln
230 235 240

Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile
245 250 255

Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val
260 265 270

Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp
275 280 285

Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His
290 295 300

Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp
305 310 315

Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys
320 325 330

Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp
335 340 345

Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro
350 355 360

Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys
365 370 375

Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn
380 385 390

Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val
395 400 405

Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp
410 415 420

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr
425 430 435

Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro
440 445 450

Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser
455 460 465

Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro
470 475 480

Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro
485 490 495

Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr
500 505 510

Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr
515 520 525

Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala
530 535 540

Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His
545 550 555

Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn
560 565 570

Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu
575 580 585

Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser
590 595 600

Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn
605 610 615

Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn
620 625 630

Ser Lys Asp Asn Val Gln Glu Thr Gln Ile
635 640

<210> 502
<211> 2458
<212> DNA
<213> Homo Sapien

<400> 502
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cgcccggcac atggctgcag ccacctcgcg cgcaccccga ggcgccgcgc 100

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agcaactgag cggggaagcg cccgcgtccg gggatcggga tgtccctcct 200

ccttctcctc ttgctagttt cctactatgt tggaaccttg gggactcaca 250

ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccaccat 300

caactggggc ttccagaaaa agacactctg gatattgaat ggctgctcac 350

cgataatgaa gggaaccaaa aagtggtgat cacttactcc agtcgtcatg 400

tctacaataa cttgactgag gaacagaagg gccgagtggc ctttgcttcc 450

aatttcctgg caggagatgc ctccttgcag attgaacctc tgaagcccag 500

tgatgagggc cggtacacct gtaaggttaa gaattcaggg cgctacgtgt 550

ggagccatgt catcttaaaa gtcttagtga gaccatccaa gcccaagtgt 600

gagttggaag gagagctgac agaaggaagt gacctgactt tgcagtgtga 650

gtcatcctct ggcacagagc ccattgtgta ttactggcag cgaatccgag 700

agaaagaggg agaggatgaa cgtctgcctc ccaaatctag gattgactac 750

aaccaccctg gacgagttct gctgcagaat cttaccatgt cctactctgg 800

actgtaccag tgcacagcag gcaacgaagc tgggaaggaa agctgtgtgg 850

tgcgagtaac tgtacagtat gtacaaagca tcggcatggt tgcaggagca 900

gtgacaggca tagtggctgg agccctgctg attttcctct tggtgtggct 950

gctaatccga aggaaagaca aagaaagata tgaggaagaa gagagaccta 1000

atgaaattcg agaagatgct gaagctccaa aagcccgtct tgtgaaaccc 1050

agctcctctt cctcaggctc tcggagctca cgctctggtt cttcctccac 1100

tcgctccaca gcaaatagtg cctcacgcag ccagcggaca ctgtcaactg 1150

acgcagcacc ccagccaggg ctggccaccc aggcatacag cctagtgggg 1200

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caaagcagaa accacaccca gcatgatccc cagccagagc agagccttcc 1300

aaacggtctg aattacaatg gacttgactc ccacgctttc ctaggagtca 1350

gggtctttgg actcttctcg tcattggagc tcaagtcacc agccacacaa 1400

ccagatgaga ggtcatctaa gtagcagtga gcattgcacg gaacagattc 1450

agatgagcat tttccttata caataccaaa caagcaaaag gatgtaagct 1500

gattcatctg taaaaaggca tcttattgtg cctttagacc agagtaaggg 1550

aaagcaggag tccaaatcta tttgttgacc aggacctgtg gtgagaaggt 1600

tggggaaagg tgaggtgaat atacctaaaa cttttaatgt gggatatttt 1650

gtatcagtgc tttgattcac aattttcaag aggaaatggg atgctgtttg 1700

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cagtcaagca gaacccacag ccttattaca cctgtctaca ccatgtactg 1800

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tctcttcttt ctgagaaaat gtgaaaccag aattgcaaga ctgggtggac 2300

tagaaaggga gattagatca gttttctctt aatatgtcaa ggaaggtagc 2350

cgggcatggt gccaggcacc tgtaggaaaa tccagcaggt ggaggttgca 2400

gtgagccgag attatgccat tgcactccag cctgggtgac agagcgggac 2450

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<210> 503
<211> 373
<212> PRT
<213> Homo Sapien

<400> 503

Met	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Val	Ser	Tyr	Tyr	Val	Gly	
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Thr	Leu	Gly	Thr	His	Thr	Glu	Ile	Lys	Arg	Val	Ala	Glu	Glu	Lys	
				20					25					30	
Val	Thr	Leu	Pro	Cys	His	His	Gln	Leu	Gly	Leu	Pro	Glu	Lys	Asp	
				35					40					45	
Thr	Leu	Asp	Ile	Glu	Trp	Leu	Leu	Thr	Asp	Asn	Glu	Gly	Asn	Gln	
				50					55					60	
Lys	Val	Val	Ile	Thr	Tyr	Ser	Ser	Arg	His	Val	Tyr	Asn	Asn	Leu	
				65					70					75	
Thr	Glu	Glu	Gln	Lys	Gly	Arg	Val	Ala	Phe	Ala	Ser	Asn	Phe	Leu	
				80					85					90	
Ala	Gly	Asp	Ala	Ser	Leu	Gln	Ile	Glu	Pro	Leu	Lys	Pro	Ser	Asp	
				95					100					105	
Glu	Gly	Arg	Tyr	Thr	Cys	Lys	Val	Lys	Asn	Ser	Gly	Arg	Tyr	Val	
				110					115					120	
Trp	Ser	His	Val	Ile	Leu	Lys	Val	Leu	Val	Arg	Pro	Ser	Lys	Pro	
				125					130					135	
Lys	Cys	Glu	Leu	Glu	Gly	Glu	Leu	Thr	Glu	Gly	Ser	Asp	Leu	Thr	
				140					145					150	
Leu	Gln	Cys	Glu	Ser	Ser	Ser	Gly	Thr	Glu	Pro	Ile	Val	Tyr	Tyr	
				155					160					165	
Trp	Gln	Arg	Ile	Arg	Glu	Lys	Glu	Gly	Glu	Asp	Glu	Arg	Leu	Pro	
				170					175					180	
Pro	Lys	Ser	Arg	Ile	Asp	Tyr	Asn	His	Pro	Gly	Arg	Val	Leu	Leu	
				185					190					195	
Gln	Asn	Leu	Thr	Met	Ser	Tyr	Ser	Gly	Leu	Tyr	Gln	Cys	Thr	Ala	
				200					205					210	
Gly	Asn	Glu	Ala	Gly	Lys	Glu	Ser	Cys	Val	Val	Arg	Val	Thr	Val	
				215					220					225	

Gln Tyr Val Gln Ser Ile Gly Met Val Ala Gly Ala Val Thr Gly
230 235 240

Ile Val Ala Gly Ala Leu Leu Ile Phe Leu Leu Val Trp Leu Leu
245 250 255

Ile Arg Arg Lys Asp Lys Glu Arg Tyr Glu Glu Glu Glu Arg Pro
260 265 270

Asn Glu Ile Arg Glu Asp Ala Glu Ala Pro Lys Ala Arg Leu Val
275 280 285

Lys Pro Ser Ser Ser Ser Ser Gly Ser Arg Ser Ser Arg Ser Gly
290 295 300

Ser Ser Ser Thr Arg Ser Thr Ala Asn Ser Ala Ser Arg Ser Gln
305 310 315

Arg Thr Leu Ser Thr Asp Ala Ala Pro Gln Pro Gly Leu Ala Thr
320 325 330

Gln Ala Tyr Ser Leu Val Gly Pro Glu Val Arg Gly Ser Glu Pro
335 340 345

Lys Lys Val His His Ala Asn Leu Thr Lys Ala Glu Thr Thr Pro
350 355 360

Ser Met Ile Pro Ser Gln Ser Arg Ala Phe Gln Thr Val
365 370

<210> 504
<211> 3060
<212> DNA
<213> Homo Sapien

<400> 504
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ccgccgccca cggcacggca gccaccatgg cgctcctgct gtgcttcgtg 100

ctcctgtgcg gagtagtgga tttcgccaga agtttgagta tcactactcc 150

tgaagagatg attgaaaaag ccaaagggga aactgcctat ctgccatgca 200

aatttacgct tagtcccgaa gaccagggac cgctggacat cgagtggctg 250

atatcaccag ctgataatca gaaggtggat caagtgatta ttttatattc 300

tggagacaaa atttatgatg actactatcc agatctgaaa ggccgagtac 350

attttacgag taatgatctc aaatctggtg atgcatcaat aaatgtaacg 400

aatttacaac tgtcagatat tggcacatat cagtgcaaag tgaaaaaagc 450

tcctggtgtt gcaaataaga agattcatct ggtagttctt gttaagcctt 500

caggtgcgag atgttacgtt gatggatctg aagaaattgg aagtgacttt 550

aagataaaat gtgaaccaaa agaaggttca cttccattac agtatgagtg 600

gcaaaaattg tctgactcac agaaaatgcc cacttcatgg ttagcagaaa 650

tgacttcatc tgttatatct gtaaaaaatg cctcttctga gtactctggg 700

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ccattatagg aactttgctt gctctagcgc tcattggtct tatcatcttt 850

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cgatatcagg gaagatgtgc cacctccaaa gagccgtacg tccactgcca 950

gaagctacat cggcagtaat cattcatccc tggggtccat gtctccttcc 1000

aacatggaag gatattccaa gactcagtat aaccaagtac caagtgaaga 1050

ctttgaacgc actcctcaga gtccgactct cccacctgct aagttcaagt 1100

acccttacaa gactgatgga attacagttg tataaatatg gactactgaa 1150

gaatctgaag tattgtatta tttgacttta ttttaggcct ctagtaaaga 1200

cttaaatgtt ttttaaaaaa agcacaaggc acagagatta gagcagctgt 1250

aagaacacat ctactttatg caatggcatt agacatgtaa gtcagatgtc 1300

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gtgacactga tagttaaaag atgttttatt atattttcaa taactaccac 1400

taacaaattt ttaacttttc atatgcatat tctgatatgt ggtcttttag 1450

gaaaagtatg gttaatagtt gatttttcaa aggaaatttt aaaattctta 1500

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cccgttcttt tccccttta tgcacacaac agaaacacgc gttgtcatgc 1600

ctcaaactat tttttatttg caactacatg atttcacaca attctcttaa 1650

acaacgacat aaaatagatt tccttgtata taaataactt acatacgctc 1700

cataaagtaa attctcaaag gtgctagaac aaatcgtcca cttctacagt 1750

gttctcgtat ccaacagagt tgatgcacaa tatataaata ctcaagtcca 1800

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tatcaatatc taaagtgcat atatttttta agaaagatta ttctcaataa 1900

cttctataaa aataagtttg atggtttggc ccatctaact tcactactat 1950

tagtaagaac ttttaacttt taatgtgtag taaggtttat tctacctttt 2000

tctcaacatg acaccaacac aatcaaaaac gaagttagtg aggtgctaac 2050

atgtgaggat taatccagtg attccggtca caatgcattc caggaggagg 2100

tacccatgtc actggaattg ggcgatatgg tttatttttt cttccctgat 2150

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cctcgataca ttcctggctt ttttctgggc aaagggtgcc acattggaag 2250

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aattcaaagg aaaaaatcat catctatgtt ccagatttct cattaaagac 2350

aaagttaccc acaacactga gatcacatct aagtgacact cctattgtca 2400

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aggccattat ccttagcaaa ctaatgcaga aacagaaaat caactaccgc 2700

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acaaaccttc atgtgtatcc ctaaacctaa aataaaagtt aaaaaaaaaa 2950

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3050

aaaaaaaaaa 3060

<210> 505
<211> 352
<212> PRT
<213> Homo Sapien

<400> 505

Met Ala Leu Leu Leu Cys Phe Val Leu Leu Cys Gly Val Val Asp
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Phe Ala Arg Ser Leu Ser Ile Thr Thr Pro Glu Glu Met Ile Glu
20 25 30

Lys Ala Lys Gly Glu Thr Ala Tyr Leu Pro Cys Lys Phe Thr Leu
35 40 45

Ser Pro Glu Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Ile Ser
50 55 60

Pro Ala Asp Asn Gln Lys Val Asp Gln Val Ile Ile Leu Tyr Ser
65 70 75

Gly Asp Lys Ile Tyr Asp Asp Tyr Tyr Pro Asp Leu Lys Gly Arg
80 85 90

Val His Phe Thr Ser Asn Asp Leu Lys Ser Gly Asp Ala Ser Ile
95 100 105

Asn Val Thr Asn Leu Gln Leu Ser Asp Ile Gly Thr Tyr Gln Cys
110 115 120

Lys Val Lys Lys Ala Pro Gly Val Ala Asn Lys Lys Ile His Leu

125 130 135

Val Val Leu Val Lys Pro Ser Gly Ala Arg Cys Tyr Val Asp Gly
140 145 150

Ser Glu Glu Ile Gly Ser Asp Phe Lys Ile Lys Cys Glu Pro Lys
155 160 165

Glu Gly Ser Leu Pro Leu Gln Tyr Glu Trp Gln Lys Leu Ser Asp
170 175 180

Ser Gln Lys Met Pro Thr Ser Trp Leu Ala Glu Met Thr Ser Ser
185 190 195

Val Ile Ser Val Lys Asn Ala Ser Ser Glu Tyr Ser Gly Thr Tyr
200 205 210

Ser Cys Thr Val Arg Asn Arg Val Gly Ser Asp Gln Cys Leu Leu
215 220 225

Arg Leu Asn Val Val Pro Pro Ser Asn Lys Ala Gly Leu Ile Ala
230 235 240

Gly Ala Ile Ile Gly Thr Leu Leu Ala Leu Ala Leu Ile Gly Leu
245 250 255

Ile Ile Phe Cys Cys Arg Lys Lys Arg Arg Glu Glu Lys Tyr Glu
260 265 270

Lys Glu Val His His Asp Ile Arg Glu Asp Val Pro Pro Pro Lys
275 280 285

Ser Arg Thr Ser Thr Ala Arg Ser Tyr Ile Gly Ser Asn His Ser
290 295 300

Ser Leu Gly Ser Met Ser Pro Ser Asn Met Glu Gly Tyr Ser Lys
305 310 315

Thr Gln Tyr Asn Gln Val Pro Ser Glu Asp Phe Glu Arg Thr Pro
320 325 330

Gln Ser Pro Thr Leu Pro Pro Ala Lys Phe Lys Tyr Pro Tyr Lys
335 340 345

Thr Asp Gly Ile Thr Val Val
350

<210> 506
<211> 1705
<212> DNA
<213> Homo Sapien

<400> 506
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ggacaagaca tgactgtgat gaggagctgc tttcgccaat ttaacaccaa 200

gaagaattga ggctgcttgg gaggaaggcc aggaggaaca cgagactgag 250

agatgaattt tcaacagagg ctgcaaagcc tgtggacttt agccagaccc 300

ttctgccctc ctttgctggc gacagcctct caaatgcaga tggttgtgct 350

cccttgcctg ggttttaccc tgcttctctg gagccaggta tcaggggccc 400

agggccaaga attccacttt gggccctgcc aagtgaaggg ggttgttccc 450

cagaaactgt gggaagcctt ctgggctgtg aaagacacta tgcaagctca 500

ggataacatc acgagtgccc ggctgctgca gcaggaggtt ctgcagaacg 550

tctcggatgc tgagagctgt taccttgtcc acaccctgct ggagttctac 600

ttgaaaactg ttttcaaaaa ccaccacaat agaacagttg aagtcaggac 650

tctgaagtca ttctctactc tggccaacaa ctttgttctc atcgtgtcac 700

aactgcaacc cagtcaagaa aatgagatgt tttccatcag agacagtgca 750

cacaggcggt ttctgctatt ccggagagca ttcaaacagt tggacgtaga 800

agcagctctg accaaagccc ttggggaagt ggacattctt ctgacctgga 850

tgcagaaatt ctacaagctc tgaatgtcta gaccaggacc tccctccccc 900

tggcactggt ttgttccctg tgtcatttca aacagtctcc cttcctatgc 950

tgttcactgg acacttcacg cccttggcca tgggtcccat tcttggccca 1000

ggattattgt caaagaagtc attctttaag cagcgccagt gacagtcagg 1050

gaaggtgcct ctggatgctg tgaagagtct acagagaaga ttcttgtatt 1100

tattacaact ctatttaatt aatgtcagta tttcaactga agttctattt 1150

atttgtgaga ctgtaagtta catgaaggca gcagaatatt gtgccccatg 1200

cttctttacc cctcacaatc cttgccacag tgtggggcag tggatgggtg 1250

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tcgccagctc accccatcat ccctttccct tggtgccctc ctttttttt 1550

tatcctagtc attcttccct aatcttccac ttgagtgtca agctgacctt 1600

gctgatggtg acattgcacc tggatgtact atccaatctg tgatgacatt 1650

ccctgctaat aaaagacaac ataactccaa aaaaaaaaaa aaaaaaaaaa 1700

aaaaa 1705

<210> 507
<211> 206
<212> PRT

<213> Homo Sapien

<400> 507

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Met Asn Phe Gln Gln Arg Leu Gln Ser Leu Trp Thr Leu Ala Arg
  1               5                  10                  15

Pro Phe Cys Pro Pro Leu Leu Ala Thr Ala Ser Gln Met Gln Met
             20                  25                  30

Val Val Leu Pro Cys Leu Gly Phe Thr Leu Leu Leu Trp Ser Gln
             35                  40                  45

Val Ser Gly Ala Gln Gly Gln Glu Phe His Phe Gly Pro Cys Gln
             50                  55                  60

Val Lys Gly Val Val Pro Gln Lys Leu Trp Glu Ala Phe Trp Ala
             65                  70                  75

Val Lys Asp Thr Met Gln Ala Gln Asp Asn Ile Thr Ser Ala Arg
             80                  85                  90

Leu Leu Gln Gln Glu Val Leu Gln Asn Val Ser Asp Ala Glu Ser
             95                 100                 105

Cys Tyr Leu Val His Thr Leu Leu Glu Phe Tyr Leu Lys Thr Val
            110                 115                 120

Phe Lys Asn His His Asn Arg Thr Val Glu Val Arg Thr Leu Lys
            125                 130                 135

Ser Phe Ser Thr Leu Ala Asn Asn Phe Val Leu Ile Val Ser Gln
            140                 145                 150

Leu Gln Pro Ser Gln Glu Asn Glu Met Phe Ser Ile Arg Asp Ser
            155                 160                 165

Ala His Arg Arg Phe Leu Leu Phe Arg Arg Ala Phe Lys Gln Leu
            170                 175                 180

Asp Val Glu Ala Ala Leu Thr Lys Ala Leu Gly Glu Val Asp Ile
            185                 190                 195

Leu Leu Thr Trp Met Gln Lys Phe Tyr Lys Leu
            200                 205
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<210> 508
<211> 924
<212> DNA
<213> Homo Sapien

<400> 508

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cggtctcagg agatgtctga tttccacaga catgcaccat atagaagaga 150

gtttccaaga aatcaaaaga gccatccaag ctaaggacac cttcccaaat 200

gtcactatcc tgtccacatt ggagactctg cagatcatta agcccttaga 250

tgtgtgctgc gtgaccaaga acctcctggc gttctacgtg gacagggtgt 300
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tcaaggatca tcaggagcca aaccccaaaa tcttgagaaa aatcagcagc 350

attgccaact ctttcctcta catgcagaaa actctgcggc aatgtcagga 400

acagaggcag tgtcactgca ggcaggaagc caccaatgcc accagagtca 450

tccatgacaa ctatgatcag ctggaggtcc acgctgctgc cattaaatcc 500

ctgggagagc tcgacgtctt tctagcctgg attaataaga atcatgaagt 550

aatgttctca gcttgatgac aaggaacctg tatagtgatc cagggatgaa 600

caccccctgt gcggtttact gtgggagaca gcccaccttg aaggggaagg 650

agatggggaa ggccccttgc agctgaaagt cccactggct ggcctcaggc 700

tgtcttattc cgcttgaaaa taggcaaaaa gtctactgtg gtatttgtaa 750

taaactctat ctgctgaaag ggcctgcagg ccatcctggg agtaaagggc 800

tgccttccca tctaatttat tgtaaagtca tatagtccat gtctgtgatg 850

tgagccaagt gatatcctgt agtacacatt gtactgagtg gtttttctga 900

ataaattcca tattttacct atga 924

<210> 509
<211> 177
<212> PRT
<213> Homo Sapien

<400> 509

Met Lys Leu Gln Cys Val Ser Leu Trp Leu Leu Gly Thr Ile Leu
1 5 10 15

Ile Leu Cys Ser Val Asp Asn His Gly Leu Arg Arg Cys Leu Ile
20 25 30

Ser Thr Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys
35 40 45

Arg Ala Ile Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu
50 55 60

Ser Thr Leu Glu Thr Leu Gln Ile Ile Lys Pro Leu Asp Val Cys
65 70 75

Cys Val Thr Lys Asn Leu Leu Ala Phe Tyr Val Asp Arg Val Phe
80 85 90

Lys Asp His Gln Glu Pro Asn Pro Lys Ile Leu Arg Lys Ile Ser
95 100 105

Ser Ile Ala Asn Ser Phe Leu Tyr Met Gln Lys Thr Leu Arg Gln
110 115 120

Cys Gln Glu Gln Arg Gln Cys His Cys Arg Gln Glu Ala Thr Asn
125 130 135

Ala Thr Arg Val Ile His Asp Asn Tyr Asp Gln Leu Glu Val His
140 145 150

Ala Ala Ala Ile Lys Ser Leu Gly Glu Leu Asp Val Phe Leu Ala

155 160 165

Trp Ile Asn Lys Asn His Glu Val Met Phe Ser Ala
170 175

<210> 510
<211> 996
<212> DNA
<213> Homo Sapien

<400> 510
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tggcttcgtt agaacgcggc tacaattaat acataacctt atgtatcata 100

cacatacgat ttaggtgaca ctatagaata acatccactt tgcctttctc 150

tccacaggtg tccactccca ggtccaactg cacctcggtt ctatcgataa 200

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gcctatccca atgcctcccc actgctcggc tccagctggg gtggcctgat 350

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tcctgtcccg gaggaacgag atccccctaa ttcacttcaa cacccccata 750

ccacggcggc acacccggag cgccgaggac gactcggagc gggacccccc 800

gaacgtgctg aagccccggg cccggatgac cccggccccg gcctcctgtt 850

cacaggagct cccgagcgcc gaggacaaca gcccgatggc cagtgaccca 900

ttaggggtgg tcaggggcgg tcgagtgaac acgcacgctg ggggaacggg 950

cccggaaggc tgccgccccc tcgccaagtt catctagggt cgctgg 996

<210> 511
<211> 251
<212> PRT
<213> Homo Sapien

<400> 511
Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys Ser
1 5 10 15

Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
20 25 30

Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala
35 40 45

Thr Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His
50 55 60

Val Asp Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile
65 70 75

Arg Ser Glu Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser
80 85 90

Arg Arg Tyr Leu Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser
95 100 105

His Tyr Phe Asp Pro Glu Asn Cys Arg Phe Gln His Gln Thr Leu
110 115 120

Glu Asn Gly Tyr Asp Val Tyr His Ser Pro Gln Tyr His Phe Leu
125 130 135

Val Ser Leu Gly Arg Ala Lys Arg Ala Phe Leu Pro Gly Met Asn
140 145 150

Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg Arg Asn Glu Ile Pro
155 160 165

Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg His Thr Arg Ser
170 175 180

Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val Leu Lys Pro
185 190 195

Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln Glu Leu
200 205 210

Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu Gly
215 220 225

Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
230 235 240

Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
245 250

<210> 512
<211> 2015
<212> DNA
<213> Homo Sapien

<400> 512
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ccggctagga tgggctgtct ctggggtctg gctctgcccc ttttcttctt 100

ctgctgggag gttggggtct ctgggagctc tgcaggcccc agcacccgca 150

gagcagacac tgcgatgaca acggacgaca cagaagtgcc cgctatgact 200

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agctctgctt cctcctacag cccctcggaa gccgccctca agaacttcac 1300

cccttcagag acaccgacca tggacatcgc aaccaagggg cccttcccca 1350

ccagcaggga ccctcttcct tctgtccctc cgactacaac caacagcagc 1400

cgagggacga acagcacctt agccaagatc acaacctcag cgaagaccac 1450

gatgaagccc caacagccac gcccacgact gcccggacga ggccgaccac 1500

agacgtgagt gcaggtgaaa atggaggttt cctcctcctg cggctgagtg 1550

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tcacatccac cggagtgtat gtatggggag gggcttcacc tgttcccaga 1900

ggtgtccttg gactcacctt ggcacatgtt ctgtgtttca gtaaagagag 1950

acctgatcac ccatctgtgt gcttccatcc tgcattaaaa ttcactcagt 2000

gtggcccaaa aaaaa 2015

<210> 513
<211> 482
<212> PRT
<213> Homo Sapien

<400> 513

Met	Gly	Cys	Leu	Trp	Gly	Leu	Ala	Leu	Pro	Leu	Phe	Phe	Phe	Cys	
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Trp	Glu	Val	Gly	Val	Ser	Gly	Ser	Ser	Ala	Gly	Pro	Ser	Thr	Arg	
				20					25					30	
Arg	Ala	Asp	Thr	Ala	Met	Thr	Thr	Asp	Asp	Thr	Glu	Val	Pro	Ala	
				35					40					45	
Met	Thr	Leu	Ala	Pro	Gly	His	Ala	Ala	Leu	Glu	Thr	Gln	Thr	Leu	
				50					55					60	
Ser	Ala	Glu	Thr	Ser	Ser	Arg	Ala	Ser	Thr	Pro	Ala	Gly	Pro	Ile	
				65					70					75	
Pro	Glu	Ala	Glu	Thr	Arg	Gly	Ala	Lys	Arg	Ile	Ser	Pro	Ala	Arg	
				80					85					90	
Glu	Thr	Arg	Ser	Phe	Thr	Lys	Thr	Ser	Pro	Asn	Phe	Met	Val	Leu	
				95					100					105	
Ile	Ala	Thr	Ser	Val	Glu	Thr	Ser	Ala	Ala	Ser	Gly	Ser	Pro	Glu	
				110					115					120	
Gly	Ala	Gly	Met	Thr	Thr	Val	Gln	Thr	Ile	Thr	Gly	Ser	Asp	Pro	
				125					130					135	
Glu	Glu	Ala	Ile	Phe	Asp	Thr	Leu	Cys	Thr	Asp	Asp	Ser	Ser	Glu	
				140					145					150	
Glu	Ala	Lys	Thr	Leu	Thr	Met	Asp	Ile	Leu	Thr	Leu	Ala	His	Thr	
				155					160					165	
Ser	Thr	Glu	Ala	Lys	Gly	Leu	Ser	Ser	Glu	Ser	Ser	Ala	Ser	Ser	
				170					175					180	
Asp	Gly	Pro	His	Pro	Val	Ile	Thr	Pro	Ser	Arg	Ala	Ser	Glu	Ser	
				185					190					195	
Ser	Ala	Ser	Ser	Asp	Gly	Pro	His	Pro	Val	Ile	Thr	Pro	Ser	Arg	
				200					205					210	
Ala	Ser	Glu	Ser	Ser	Ala	Ser	Ser	Asp	Gly	Pro	His	Pro	Val	Ile	
				215					220					225	
Thr	Pro	Ser	Trp	Ser	Pro	Gly	Ser	Asp	Val	Thr	Leu	Leu	Ala	Glu	
				230					235					240	
Ala	Leu	Val	Thr	Val	Thr	Asn	Ile	Glu	Val	Ile	Asn	Cys	Ser	Ile	
				245					250					255	

Thr Glu Ile Glu Thr Thr Thr Ser Ser Ile Pro Gly Ala Ser Asp
260 265 270

Ile Asp Leu Ile Pro Thr Glu Gly Val Lys Ala Ser Ser Thr Ser
275 280 285

Asp Pro Pro Ala Leu Pro Asp Ser Thr Glu Ala Lys Pro His Ile
290 295 300

Thr Glu Val Thr Ala Ser Ala Glu Thr Leu Ser Thr Ala Gly Thr
305 310 315

Thr Glu Ser Ala Ala Pro His Ala Thr Val Gly Thr Pro Leu Pro
320 325 330

Thr Asn Ser Ala Thr Glu Arg Glu Val Thr Ala Pro Gly Ala Thr
335 340 345

Thr Leu Ser Gly Ala Leu Val Thr Val Ser Arg Asn Pro Leu Glu
350 355 360

Glu Thr Ser Ala Leu Ser Val Glu Thr Pro Ser Tyr Val Lys Val
365 370 375

Ser Gly Ala Ala Pro Val Ser Ile Glu Ala Gly Ser Ala Val Gly
380 385 390

Lys Thr Thr Ser Phe Ala Gly Ser Ser Ala Ser Ser Tyr Ser Pro
395 400 405

Ser Glu Ala Ala Leu Lys Asn Phe Thr Pro Ser Glu Thr Pro Thr
410 415 420

Met Asp Ile Ala Thr Lys Gly Pro Phe Pro Thr Ser Arg Asp Pro
425 430 435

Leu Pro Ser Val Pro Pro Thr Thr Thr Asn Ser Ser Arg Gly Thr
440 445 450

Asn Ser Thr Leu Ala Lys Ile Thr Thr Ser Ala Lys Thr Thr Met
455 460 465

Lys Pro Gln Gln Pro Arg Pro Arg Leu Pro Gly Arg Gly Arg Pro
470 475 480

Gln Thr

<210> 514
<211> 2284
<212> DNA
<213> Homo Sapien

<400> 514
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ggcgccgggg tcctctcgac gccagagaga aatctcatca tctgtgcagc 150

cttcttaaag caaactaaga ccagagggag gattatcctt gacctttgaa 200

gaccaaaact aaactgaaat ttaaaatgtt cttcgggggga gaagggagct 250

tgacttacac tttggtaata atttgcttcc tgacactaag gctgtctgct 300

agtcagaatt gcctcaaaaa gagtctagaa gatgttgtca ttgacatcca 350

gtcatctctt tctaagggaa tcagaggcaa tgagcccgta tatacttcaa 400

ctcaagaaga ctgcattaat tcttgctgtt caacaaaaaa catatcaggg 450

gacaaagcat gtaacttgat gatcttcgac actcgaaaaa cagctagaca 500

acccaactgc tacctatttt tctgtcccaa cgaggaagcc tgtccattga 550

aaccagcaaa aggacttatg agttacagga taattacaga ttttccatct 600

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tccaacttaa ctttgaacac agggaatgtg tataacccta ctgcactttc 1250

tatgtcaaat gtggagtctt ccactatgaa taaaactgct tcctgggaag 1300

gtagggaggc cagtccaggc agttcctccc agggcagtgt tccagaaaat 1350

cagtacggcc ttccatttga aaaatggctt cttatcgggt ccctgctctt 1400

tggtgtcctg ttcctggtga taggcctcgt cctcctgggt agaatccttt 1450

cggaatcact ccgcaggaaa cgttactcaa gactggatta tttgatcaat 1500

gggatctatg tggacatcta aggatggaac tcggtgtctc ttaattcatt 1550

tagtaaccag aagcccaaat gcaatgagtt tctgctgact tgctagtctt 1600

agcaggaggt tgtattttga agacaggaaa atgccccctt ctgctttcct 1650

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tagcacgatc tcggctctca ccgcaacctc cgtctcctgg gttcaagcga 1750

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acacctgggt gatttttgta tttttagtag agacggggtt tcaccatgtt 1850

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cccaaagtgc tgggattaca ggcatgagcc accacagctg gccccttct 1950

gttttatgtt tggtttttga gaaggaatga agtgggaacc aaattaggta 2000

attttgggta atctgtctct aaaatattag ctaaaaacaa agctctatgt 2050

aaagtaataa agtataattg ccatataaat ttcaaaattc aactggcttt 2100

tatgcaaaga aacaggttag gacatctagg ttccaattca ttcacattct 2150

tggttccaga taaaatcaac tgtttatatc aatttctaat ggatttgctt 2200

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<210> 515
<211> 431
<212> PRT
<213> Homo Sapien

<400> 515

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Ile	Cys	Phe	Leu	Thr	Leu	Arg	Leu	Ser	Ala	Ser	Gln	Asn	Cys	Leu	
			20					25						30	
Lys	Lys	Ser	Leu	Glu	Asp	Val	Val	Ile	Asp	Ile	Gln	Ser	Ser	Leu	
			35					40						45	
Ser	Lys	Gly	Ile	Arg	Gly	Asn	Glu	Pro	Val	Tyr	Thr	Ser	Thr	Gln	
			50					55						60	
Glu	Asp	Cys	Ile	Asn	Ser	Cys	Cys	Ser	Thr	Lys	Asn	Ile	Ser	Gly	
			65					70						75	
Asp	Lys	Ala	Cys	Asn	Leu	Met	Ile	Phe	Asp	Thr	Arg	Lys	Thr	Ala	
			80					85						90	
Arg	Gln	Pro	Asn	Cys	Tyr	Leu	Phe	Phe	Cys	Pro	Asn	Glu	Glu	Ala	
			95					100						105	
Cys	Pro	Leu	Lys	Pro	Ala	Lys	Gly	Leu	Met	Ser	Tyr	Arg	Ile	Ile	
			110					115						120	
Thr	Asp	Phe	Pro	Ser	Leu	Thr	Arg	Asn	Leu	Pro	Ser	Gln	Glu	Leu	
			125					130						135	
Pro	Gln	Glu	Asp	Ser	Leu	Leu	His	Gly	Gln	Phe	Ser	Gln	Ala	Val	
			140					145						150	
Thr	Pro	Leu	Ala	His	His	His	Thr	Asp	Tyr	Ser	Lys	Pro	Thr	Asp	
			155					160						165	
Ile	Ser	Trp	Arg	Asp	Thr	Leu	Ser	Gln	Lys	Phe	Gly	Ser	Ser	Asp	
			170					175						180	
His	Leu	Glu	Lys	Leu	Phe	Lys	Met	Asp	Glu	Ala	Ser	Ala	Gln	Leu	
			185					190						195	

Leu Ala Tyr Lys Glu Lys Gly His Ser Gln Ser Ser Gln Phe Ser
200 205 210

Ser Asp Gln Glu Ile Ala His Leu Leu Pro Glu Asn Val Ser Ala
215 220 225

Leu Pro Ala Thr Val Ala Val Ala Ser Pro His Thr Thr Ser Ala
230 235 240

Thr Pro Lys Pro Ala Thr Leu Leu Pro Thr Asn Ala Ser Val Thr
245 250 255

Pro Ser Gly Thr Ser Gln Pro Gln Leu Ala Thr Thr Ala Pro Pro
260 265 270

Val Thr Thr Val Thr Ser Gln Pro Pro Thr Thr Leu Ile Ser Thr
275 280 285

Val Phe Thr Arg Ala Ala Ala Thr Leu Gln Ala Met Ala Thr Thr
290 295 300

Ala Val Leu Thr Thr Thr Phe Gln Ala Pro Thr Asp Ser Lys Gly
305 310 315

Ser Leu Glu Thr Ile Pro Phe Thr Glu Ile Ser Asn Leu Thr Leu
320 325 330

Asn Thr Gly Asn Val Tyr Asn Pro Thr Ala Leu Ser Met Ser Asn
335 340 345

Val Glu Ser Ser Thr Met Asn Lys Thr Ala Ser Trp Glu Gly Arg
350 355 360

Glu Ala Ser Pro Gly Ser Ser Ser Gln Gly Ser Val Pro Glu Asn
365 370 375

Gln Tyr Gly Leu Pro Phe Glu Lys Trp Leu Leu Ile Gly Ser Leu
380 385 390

Leu Phe Gly Val Leu Phe Leu Val Ile Gly Leu Val Leu Leu Gly
395 400 405

Arg Ile Leu Ser Glu Ser Leu Arg Arg Lys Arg Tyr Ser Arg Leu
410 415 420

Asp Tyr Leu Ile Asn Gly Ile Tyr Val Asp Ile
425 430

<210> 516
<211> 2749
<212> DNA
<213> Homo Sapien

<220>
<221> unsure
<222> 1869, 1887
<223> unknown base

<400> 516
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gcgggttcga aggggacact gtgtccctgc agtgcaccta cagggaagag 150

ctgagggacc accggaagta ctggtgcagg aagggtggga tcctcttctc 200

tcgctgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250

agggcagggt gtccatccgt gacagccgcc aggagctctc gctcattgtg 300

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acaacacgcc tgcagcccaa ggcaaaagct cagcaaaccc agcccccagg 500

attgacttct cctgggctct acccggcagc caccacagcc aagcagggga 550

agacaggggc tgaggcccct ccattgccag ggacttccca gtacgggcac 600

gaaaggactt ctcagtacac aggaacctct cctcacccag cgacctctcc 650

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tcacgcttga ctgcggagga aaaggaagcc ccttcccagg cccctgaggg 950

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tctcgaagtt tgtctcagcg tagggcagga ggccctcctg gccaggccag 1050

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gagtagctgg gattacaggc acgcaccacc acacctggct aatttttgta 2300

cttttagtag agatggggtt tcaccatgtt ggccaggctg gtcttgaact 2350

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tttgttgtac ttccttccac tcttttcttc ttcacataat ttgccggtgt 2600

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tccaccttat cgttccatca ctttattcca gcacttctct gtgttttaca 2700

gacctttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaa 2749

<210> 517
<211> 332
<212> PRT
<213> Homo Sapien

<400> 517

Met	Arg	Leu	Leu	Val	Leu	Leu	Trp	Gly	Cys	Leu	Leu	Leu	Pro	Gly	
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Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu	Gly	
				20				25						30	
Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg	Asp	
				35				40						45	
His	Arg	Lys	Tyr	Trp	Cys	Arg	Lys	Gly	Gly	Ile	Leu	Phe	Ser	Arg	
				50				55						60	
Cys	Ser	Gly	Thr	Ile	Tyr	Ala	Glu	Glu	Glu	Gly	Gln	Glu	Thr	Met	
				65				70						75	

Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu
80 85 90

Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr
95 100 105

Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile
110 115 120

Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser
125 130 135

Pro Thr Phe Gln Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala
140 145 150

Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu
155 160 165

Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu
170 175 180

Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr
185 190 195

Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro
200 205 210

Ala Gly Ser Ser Arg Pro Pro Met Gln Leu Asp Ser Thr Ser Ala
215 220 225

Glu Asp Thr Ser Pro Ala Leu Ser Ser Gly Ser Ser Lys Pro Arg
230 235 240

Val Ser Ile Pro Met Val Arg Ile Leu Ala Pro Val Leu Val Leu
245 250 255

Leu Ser Leu Leu Ser Ala Ala Gly Leu Ile Ala Phe Cys Ser His
260 265 270

Leu Leu Leu Trp Arg Lys Glu Ala Gln Gln Ala Thr Glu Thr Gln
275 280 285

Arg Asn Glu Lys Phe Trp Leu Ser Arg Leu Thr Ala Glu Glu Lys
290 295 300

Glu Ala Pro Ser Gln Ala Pro Glu Gly Asp Val Ile Ser Met Pro
305 310 315

Pro Leu His Thr Ser Glu Glu Glu Leu Gly Phe Ser Lys Phe Val
320 325 330

Ser Ala

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 518

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<210> 519
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 519
ctgtcttccc ctgcttggct gtgg 24

<210> 520
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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ggtgcaggaa gggtgggatc ctcttctctc gctgctctgg ccacatc 47

<210> 521
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 521
ccagtgcaca gcaggcaacg aagc 24

<210> 522
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 522
actaggctgt atgcctgggt gggc 24

<210> 523
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 523
gtatgtacaa agcatcggca tggttgcagg agcagtgaca ggc 43

<210> 524
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 524
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<210> 525
<211> 25
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<220>
<223> Synthetic oligonucleotide probe

<400> 525
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<210> 526
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<220>
<223> Synthetic oligonucleotide probe

<400> 526
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<210> 527
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 527
gatgaacttg gcgaaggggc ggca 24

<210> 528
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 528
agggaggatt atccttgacc tttgaagacc 30

<210> 529
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 529
gaagcaagtg cccagctc 18

<210> 530
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Replacement Sheet - EP 2 258 860